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Perfect score:

Sequence:

Scoring table:

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61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Acton, Susan L.
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOWOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
STREET: One Post Office Square
CITY: Boston
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STATE: MA

COMPTRY: USA

ZOT109-2170

ZOT109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREADIN Release #1.0, Version #1.30

SOFTWARE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: IBM PC-1997

CLASSIFICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997

CLASSIFICATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MIA-025.01

TELEPHONE: 617-832-1000

TELEPHONE: 617-832-1000
                                  US-09-407-427-6
US-09-635-501-6
US-08-98-299-10
US-08-98-299-10
US-09-635-501-10
US-09-635-501-11
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US-09-635-501-11
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Patent No. 6194556
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Best Local Similarity 100.
Matches 595; Conservative
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; MOLECULE TYPE: protein
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Sequence 140, App
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Sequence 138, App
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                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-635-501-106

US-10-158-825-142

US-10-158-825-144

US-10-158-847-140

US-10-158-847-138

US-10-158-847-138

US-10-158-825-14

US-10-158-825-14

US-08-407-427-4

US-09-635-501-4

US-09-635-501-7

US-09-635-501-7

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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Acton, Susan L.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME
TITLE REFERENCE: MANGER: US/09/407,427
CURRENT PILLING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR PILLING DATE: 1998-09-10
PRIOR PILLING DATE: 1998-01-10
RUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 2.8e-309;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 595; Conservative
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US-09-407-427-2
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TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REFERENCE: PFS57
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,004
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 142
LENGTH: 805
                                                                                                                                                                       199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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Patent No. 6592865
GENERAL INFORMATION:
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; ORGANISM: homo sapiens
US-10-158-847-142
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APPLICANT: Accon, Susan L. et al.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC;
TITLE OF INVENTION: DAGNOSTIC USES THEREFOR
FILE REFERENCE: MNI-132CP3;
CURRENT APPLICATION NUMBER: US/09/635,501
CURRENT APPLICATION NUMBER: US/09/635,501
FRIOR APPLICATION NUMBER: 09/407,427
PRIOR PILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-39
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS: 107
DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
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                                                                                                                                                                 439 LLKQALTIVGTLPPTYMLEKWRRWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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                                                                                              19 STIEEGAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEBNVQNMNAGDKWSAFLKEQST
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                                                                                                                                               LLKQALTIVGTLPFTYMLEKWRWWVFKGBIPKDQWMKKWWEMKRBIVGVVBPVPHDBTYC
                                                                       1QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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100.0%; Score 3231; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.8e-309;
Matches 595; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106, Application US/09635501; Patent No. 6884771; GENERAL INFORMATION:
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CRGANISM: Homo sapiens
US-09-635-501-106
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US-09-635-501-106
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US-09-635-501-2

Sequence 2, Application US/09635501

Fatent No. 6884711

GENERAL INFORMATION:

APPLICANT: Acton, Susan L. et al.

APPLICANT: Acton, Susan L. et al.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC

TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR

FILE REFERENCE: MNI-132CP3

CURRENT APPLICATION NUMBER: US/09/635,501

CURRENT FILING DATE: 1999-09-29

PRIOR PILING DATE: 1999-09-29

PRIOR FILING DATE: 1998-09-29

PRIOR FILING DATE: 1998-09-30

PRIOR FILING DATE: 1998-09-30

PRIOR SPLICATION NUMBER: 08/989,299

PRIOR SPLICATION NUMBER: 08/989,299

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn Ver. 2.0
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259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKBAEKFFVSV 318
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                                                                                                                                                379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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                                                      GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                              I QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPXHLKSIGLLSPDFQEDNETEINF
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ORGANISM: Homo sapiens
US-09-635-501-2
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Sequence 11284, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEBSESEQ for Windows Version 4.0
SEQ ID NO 11284
LENGTH: 819
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 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                      33 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                                            559 RIGKSEPWILALENVVGAKNMVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
                                                                     541 RIGKSEPWTLALENVVGAKNMNVRPLLINYFEPLFTWLKDONKNSFVGWSTDWSPY
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100.0%; Score 3231; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.9e-309;
Matches 595; Conservative 0; Mismatches 0;
                                                                                                                                                                RESULT 7
US-09-949-016-11284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                  Sequence 142, Application US/10158825
Sequence 142, Application US/10158825
Patent No. 6900033
GENERAL INFORMATION:
APPLICANT TOM Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REPERENCE: PP555
CURRENT APPLICATION NUMBER: US/10/158,825
CURRENT APPLICATION NUMBER: 60/294,976
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
LENGTH: 805
                      379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                            STIEEQAKTFLDKFNHEAEDLFYQSSLASWYNTNITEENVQNMNAGDKWSAFLKEQST
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 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                       LIKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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100.0%; Pred. No. 2.8e-309;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 595; Conservative
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; ORGANISM: homo sapiens
US-10-158-825-142
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                                                                                                                                                                                                                               Sequence 140. Application US/10158825
; Sequence 140. Application US/10158825
; Patent No. 6900033
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PFS55
; CURRENT PILING DATE: 2002-06-03
; PRIOR PILING DATE: 2001-06-04
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 140
; LENGTH: 681
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99.3%; Pred. No. 2.5e-285;
iive 0; Mismatches 4;
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ORGANISM: homo sapiens
PEATURE:
IOCATION: (2197...(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
IOCATION: (240)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
IOCATION: (4997...(499)
COTHER INFORMATION: Xaa equals any amino acid
FEATURE:
OTHER INFORMATION: Xaa equals any amino acid
OTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-140
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Matches 548; Conservative
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US-10-158-825-140
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  513 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 572
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                                                                                                                                                            Patent No. 6592865
GENERAL INFORMATION
PATENT NO. 6592865
GENERAL INFORMATION
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REFERENCE: PFS57
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 140
LENGTH: 681
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                                                          573 RLGKSEPWTLALENVVGAKNMVVRPLLNYFEPLFTWLKDQNKNSFVGMSTDWSPY 627
                                      541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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NAME/KEY: MISC_FEATURE
LOCATION: (219)..(219)
OTHER INFORMATION: Xaa equals any amino acid
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LOCATION: (4997...(499)
CTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140
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NOME/KRY: MISC. FEATURE
LOCATION: (240)
OTHER INFORMATION: Xaa equals
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ORGANISM: homo sapiens
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301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
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TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REPERENCE: PP555
CURRENT APPLICATION NUMBER: US/10/158,825
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 138
                                                                                                                                                                                                  GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMK
                                                      361 GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWAVFKGEIPKDQWMKKWWWEMK
                                                                                                                             421 REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
                                                                                                                                                                              CDISNSTEAGQXLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKN
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                                                                                                        REIVGVVEPVPHDETYCDPASLFHVSNDXSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
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NAME/KEY: MISC FEATURE
NAME/KEY: (219)...(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
NAME/KEY: (240)...(240)
OTHER INFORMATION: Xaa equals any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (499)...(499)
TOTHER INFORMATION: Xaa equals any amino acid
US-10-158-825-138
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US-10-158-825-138
Sequence 138, Application US/10158825; Patent No. 6900033; GENERAL INFORMATION:
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ORGANISM: homo sapiens
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Matches 548;
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GLLSPDFQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMK 420
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                                                                                                                                                                                                                                                                                                Sequence 138, Application US/10158847
Patent No. 6592865
GENERAL INFORMATION
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity FILE REPERENCE: PFEST
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
LENGTH: 711
                                   REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHK
                                                        REIVGVVEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQFQEALCQAAKHEGPLHK
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Pred. No. 2.7e-285;
0; Mismatches 4;
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NAME/KEY: MISC_FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa equals any amino acid
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Best Local Similarity 99.3
Matches 548; Conservative
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OTHER INFORMATION: Xaa
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TANN: (219)...(219)
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ORGANISM: homo sapiens
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NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 RANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNA 233
                                                                                                                                                                                                                                                                    | | :| |::::: :: :: : |:||||||| | |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| 
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Patent No. 6194556;
GENERAL INFORMATION:
APPLICANT: Robinson, Keith E.
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                         34;
                                                                                             Length 732;
                                                                                                                                                            IndelB
                                                                                             Query Match
41.3%; Score 1335; DB 1;
Best Local Similarity 41.9%; Pred. No. 2.4e-122;
Matches 254; Conservative 116; Mismatches 202;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
; MOLECULE TYPE: protein US-08-481-626-2
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STATE: MA
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APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Alhenc-Gelas, Francois
APPLICANT: Hubert, Christine
APPLICANT: Corvol, Pierre
TITLE OF INVENTION: Nucleic Acid Coding for the Human
TITLE OF INVENTION: Testicular Angiotensin Converting Enzyme (ACE) and its
TITLE OF INVENTION: Uses, Especially for the In Vitro Screening for this
TITLE OF INVENTION: Brayme in the Organism
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
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                                                                                                    301 TKVTMDDFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSI 360
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                                                                                                                                                                                                                               GLLSPDFQEDNETEINFLLKQALTIVGTLPPTYMLEXWRWNVFKGEIPKDQWMKKWWEMK 420
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241 WDAQRIFKEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300
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                                                               TKVTMDDFLTAHHEMGH1QYDMAYAAQPFLLRNGANEGFHEAVGB1MSLSAATPKHLKS1
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CITY: Washington
STATE: 1300 I Street, N.W., Suite 700
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
SOFTWARR: Patentin Release #1.0, Version #1.25
GONTWARR: Patentin Release #1.0, Version #1.25
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US /08/481,626
FILING DATE: 04-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION AMR-1991
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: R 89-09062
FILING DATE: 05-UUL-1999
ATFONEY/AGENT INFORMATION:
WANNER MADEL CATALLING BATA:
APPLICATION NUMBER: FR 89-09062
FILING DATE: 05-UUL-1999
ATFONEY/AGENT INFORMATION:
WANNER MADEL CATALLING BATE: 05-UUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
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RECISTRATION NUMBER: 25,146
REPERENCE, DOCKET NUMBER: 04958-0006-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08481626
Patent No. 5801040
GENERAL INFORMATION:
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LENGTH: 732 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 732;
                                               APPLICANT: Acton, Susan L.
APPLICANT: Robison, Keitch E.
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
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41.3%; Score 1335; DB 2;
Best Local Similarity 41.9%; Pred. No. 2.4e-122;
Matches 254; Conservative 116; Mismatches 202;
                                                                                                                                                   FILE REFERENCE: MNI-132CP2
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR PELING DATE: 1998-09-30
PRIOR PELING DATE: 1998-09-30
PRIOR PELING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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US-09-635-501-4
; Sequence 4, Application US/09635501
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ORGANISM: Homo sapiens
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                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4
LENGTH: 732
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182 VCHPNG--SCLQLEPDLTNVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQAA
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SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION.
FILING DATE: 11-L.
FILING DATE: 11-L.
CLASSIFICATION: 514
ATTORNEY/AGRAT INFORMATION:
NAME: Arnold E. Beth
REGISTRATION NUMBER: 35,430
REPRENCE/DOCKET NUMBER: MIA-025.01
TELECHMUNICATION INFORMATION:
TELEPRAX: 617-832-1000
TELEPRAX: 617-832-1000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRACTERISTICS:
LENGTH: 732 amino acids
"VPE: amino acids
"VPE: amino acids
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        11-DEC-1997
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US-09-407-427-4
; Sequence 4, Application US/09407427
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Best Local Similarity
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acton, Sugan L. et al.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR
FILE REFERENCE: MNI-132CP3
CURRENT APPLICATION NUMBER: US/09/635,501
CURRENT FILING DATE: 200-08-09
PRIOR APPLICATION NUMBER: 09/407,427
PRIOR APPLICATION NUMBER: 09/407,427
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR RILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTING VAICE: 2.0
SEQ ID NO 4
LENGTH: 732
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41.3%; Score 1335; DB 2; Length 732;
Best Local Similarity 41.9%; Pred. No. 2.4e-122;
Matches 254; Conservative 116; Mismatches 202; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-635-501-4
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The present invention relates to a crystal (I) comprising an angiotensin-
converting enzyme-related carboxypeptidase (ACE2) or its homolog. (I) is
useful for detecting chemical compounds such as ligand, antagonist,
agonist, inhibitor, antibody, peptide, protein or drug having capability
of binding to the active site of the ACE2 protein. The present sequence
is human ACE2, used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crystal of angiotensin-converting enzyme-related carboxypeptidase or its homolog, useful for detecting compounds e.g. ligands capable of binding to angiotensin-converting enzyme-related carboxypeptidase.
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ABU80905
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Towler PS, Williams
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- 2006 Biocceleration Ltd.
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                                                                 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                                                                                                         QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED
                                                                                                                                                                       121 QECLILEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
                                                                                                                                                                                                          YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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                                                  STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIGKSEPWTLALENVVGAKOMNVRPLLINYFEPLFTWLKDONKNSFVGWSTDWSPY
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                         Indels
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            Pred. No. 3.8e-288;
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100.08;
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            Best Local Similarity 100.
Matches 595; Conservative
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12-SEP-2002;
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Harthshorne 1
Mooney EM, I
Stevens KA,
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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A purint cleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. call proliferative disorders, endocrine disorder, neurological disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp infections caused by virus, bacteria, fungi or parasite. The dithp promethisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline constitution. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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ioux P, Shen EJ, Wu MC, Stuve LL;
rt EA, Wingrove J, Vitt UA, Kirton ES;
Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
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                                                                                                                                             New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QECLILEPGINEIMANSLDYNERLWAMESWRSEVGKQLRPLYEBYYVLKNEMARANHYED
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100.0%; Pred. No. 5.7e-288;
ive 0; Mismatches 0;
Anderson SB, Rioux P,
Spiro PA, Stewart EA, W
g M, Policky JL, Hurwitz
Shi X, Suarez CJ;
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                                   Kwong M, Po
S, Shi X,
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N-PSDB; ACN43791.
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Peralta CH,
                  Lagace RE,
Xu Y, Kwo
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                                                                                         QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEWARANHYED
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                                                                      LAQMYPLQBIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
                                                                                                                                              QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
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STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MPROT15 amino acid sequence #1.
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18-AUG-1998;
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                                                                                                                                                                                                                                                                         Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang. (1-9); blood pressure; hypertension; congestive heart failure; atherosclerosis; chronic heart failure; acute heart failure; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2) polypeptide useful for detecting an ACE-2 therapeutic for treating hypertension, congestive heart failure, myocardial infarction, atherosclerosis and renal failure.
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                                                                                                                                                                                                                                         A human angiotensin converting enzyme-2 (ACB-2) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "minimal zinc binding domain"
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766. .805
/note= "cytoplasmic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "extracellular domain"
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N-PSDB; AAA12764.
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Homo sapiens.

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                                                                   treatment of
                                                 This is amino acid sequence #1 of human MPROTIS. The MPROTIS polynucleotide and polypeptide sequences can be used for the treatment of Myperension, myocardial diseases, apoplexy, heart diseases, nervous denaturation, Alzheimer's disease and diseases related to the processing of peptide hormones and cytokines
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myocardial diseases, apoplexy, heart diseases,
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100.0%; Pred. No. 6.1e-288;
iive 0; Mismatches 0;
          nervous denaturation, Alzheimer's disease etc.
                               Page 15; 22pp; Japanese.
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hypertension,
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The invention relates to the metalloenzyme Zace2. Zace2, an angiotensin-
converting enzyme is a zinc metallopeptidase that plays roles in blood
pressure regulation and fertility. Zace2 can be expressed by standard
recombinant methodology. Zace2 polypeptides are useful for treating an
inflammatory bowel disease (e.g. Crohn's disease and ulcerative colitis),
diseases associated with inflammation like arthritis and entercolitis,
as targets for identifying modulators of zinc protease activity, for
careening or identifying new angiotensin-converting enzyme (ACB)
inhibitors, and as a basis for rational drug design for inhibitory
molecules. The nucleic acide can be used to detect the expression of a
cace2 gene in a biological sample, as probes for in vivo diagnosis and
for detecting and localizing Zace2 gene expression in tissue samples, to
determine whether a subject's chromosomes contain a mutation in the Zace2
gene, and to detect aberrations associated with the Zace2 locus.
Inhibitors of ACB are used for treating hypertension of various
conditions, including left ventricular systolic dysfunction, progressive
cenal impairment, solaroderma renal crisis, congestive heart failure due
to dysfunction, and treatment of atherosclerosis. Zace2 agonists may be
used to treat infertility while Zace2 antagonists are used for inducing
infertility. The present sequence represents the human Zace2 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin-converting enzyme, Zace2, useful for treating inflammatory bowel disease, e.g. Crohn's disease and ulcerative colitis, or diseases associated with inflammation such as arthritis and enterocolitis.
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100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       Shoemaker KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 95-100; 125pp; English.
                                                                                                                             03-MAY-2000; 2000WO-US011932.
                                                                                                                                                                                        99US-00311482.
99US-00384706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC84366, AAC84367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595; Conservative
                                                                                                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                               2001-025018/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 805 AA;
                                                                                                                                                                                                                                                                                                                                                       Piddington CS,
WO200070032-A1
                                                                                                                                                                                            13-MAY-1999;
                                                                                                                                                                                                                         27-AUG-1999;
                                                           23-NOV-2000
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for sequence specific modulation of gene expression or in the analysis of single base-pair mutations in the gene. Nucleic acid sequence encoding TEE2 is useful in therapeutics, diagnostics and in screening assays. ACE 2 antagonist is used to treat hypertension or congestive heart failure (CHF). ACE agonist is used to reduce the inflammation and pain resulting from an insect sting or bite, which was accompanied by an injection of bradykinin. Anti-ACE-2 antibodies are used to monitor ACE-2 protein abserrant protein level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; angiotensin converting enzyme-2; ACE-2; therapy; hypertension; peptidyl dipeptidase A; blood pressure; hypotension; atherosclerosis; myocardial infarction; heart failure; arrhythmia; renal failure; gene; inflammation; fertility; enzyme; BC 3.4.15.1.
                                                                                                                                                                                                                                                                                         LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
                                                                                                                                                                                                                                                                                                         QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED
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                                                                                                                                                                                                                                                    STIEEQAKTFLDKFNHEAEDLFYQSSLASWYNTNITEENVQNMNNAGDKWSAFLKEQST
                                                                                                                                                                                                                                                                                                                                                QECLILLEPGLINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEBYVVLKNEMARANHYED
                                                                                                                                                                                                                                                                                                                                                                                                        YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPASLFHVSNDYSFIRYYTRTLYQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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                                                                                                                                                                         Length 805;
                                                                                                                                                                                                     Indels
                                                                                                                                                                        100.0%; Score 3231; DB 4;
100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ACE-2 full-length protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)<sup>3</sup>
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                        Local Similarity
les 595; Conser
                                                                                                                                                 Sequence 805 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                           Query Match
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                                                                                                      LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480
                                                                                                                     540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present amino acid sequence is human angiotensin converting enzyme-2 (ACE-2), also referred as peptidyl dipeptidase A (EC 3.4.15.1). Nucleic acid sequence encoding ACE-2 is useful as antisense or antigene agents
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą;
                                                             DPASLFHVSNDYSF1RYYTRTLYQFQFQEALCQAAKHEGPLHKCD1SNSTEAGQKLFNML
                                                                                                                                                                                                                                    RIGKSEPWTLALENVVGAKNMVVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                 angiotensin converting enzyme-2, ACE-2; peptidyl dipeptidase ing; therapy; hypertension; congestive heart failure; CHF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Transmembrane domain; Hydrophobic region"
                                                                                                                                                                                                                    RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes encoding angiotensin converting enzyme-2 useful as igene agents for therapeutics, diagnostics and screening
                                                                                                                                                                                                                                                                                                                                                                                                        Human angiotensin converting enzyme-2 (ACE-2)
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/label= Mature_ACE-2_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Zinc binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           766. .805
/label= Cytoplasmic_domain
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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                                                                                                                                                                                                                                                                                                                   AAY72667 standard; protein; 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374. .378
/label= ZBD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 33; Fig 1; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-210604/21.
N-PSDB; AAD02758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening; therapy; inflammation; pain.
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                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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438 480 498 558

595

us-10-659-000-4.rag

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Aminopeptidase P; XPNEP2; bradykinin receptor B1; BDKRB1; tachykinin receptor B1; TACR1; C1 esterase inhibitor; C1NH; kallikrein 1; K1K1; bradykinin receptor B2; BDKRB2; gene therapy; and addykinin receptor B2; BDKRB2; gene therapy; and converting enzyme 2; ACE2; protease inhibitor 4; P14; angiotensin converting enzyme 2; ACE2; protease inhibitor 4; P14; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; encuryam; embolism; thrombosis; coronary artery disease; angioedaema; autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; chronic obstructive pulmonary disease; enterocolitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid with at least one polymorphic position, useful for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and
                                                                                                                                                                               GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                  319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                        IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                               379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                     LLKOALTIVGTLPFTYMLEKWRWWPKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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                                                                                                                                                                                                                                                                                                                                 RLGKSEPWTLALENVVGAKNMNVRPLLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiotensin converting enzyme 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 32; 977pp; English
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23-JAN-2001; 2001US-0263678P.
02-MAR-2001; 2001US-0273037P.
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Swanson BN, Powell JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSUCHIHASHI Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-619265/66.
N-PSDB; ABS60372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200261131-A2.
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(HUIL/) HUI L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG77011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human angiotensin converting enzyme-2 (ACE-2) polypeptides and polynucleotides. ACE-2 is also known as peptidyl dispeptidase A (EC 3.4.15.1). Polypeptides of the invention are useful for treating or preventing the development of abnormal blood pressure and diseases or disorders associated with the protein in a subject. The diseases include hypertension, hypotension, congestive heart failure, chronic heart failure, acute heart failure, mycoardial infarction, atherosclerosis, arrhythmia and renal failure. They are also useful for treating inflammatory conditions and diseases relating to fertility. The present sequence is human full-length ACE-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human polypeptide, known as angiotensin converting enzyme-2, useful for treating or preventing the development of an abnormal blood pressure or related diseases, e.g. hypertension, heart failure or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTTYSTGKVCNPDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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0
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                                                                                                                                     /note= "Zinc binding domain (ZBD)" 741. .765
                                                                                                                                                         741. .765
/note= "Transmembrane domain"
766. .805
                                                                                                             /note= "Extracellular domain" 374. .378
                                                                            "Mature ACE-2 protein"
                                                                                                                                                                                                                                      'note= "Cytoplasmic domain"
                  1. .18
/label= Signal_peptide
  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hsieh FY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Fig 1; 218pp; English
                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001; 2001WO-US025059.
                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2000; 2000US-00635501
                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC.
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                                                            .805
                                                                                /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robison KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD32586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 805 AA;
                                                                                                                                                                                                                                                                          WO200212471-A2
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    Key
Peptide
                                                          Protein
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                                                                                                                                                                             Domain
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The invention relates to an isolated nucleic acid from a human gene anceding aminopeptidase P (XPNRE2), bradykinin receptor B1 (TRACH), C1 esterase inhibitor (C1MH), kallikrein techpotor B1 (TRACH), C1 esterase inhibitor (C1MH), kallikrein (C2 (ACES)) or protease inhibitor 4 (1914), comprising at least one captor B2 (ACES) or protease inhibitor 4 (1914), comprising at least one composition as provided in the detailed summary of single polymorphic position as provided in the detailed summary of single conclains comprising additional 5' and 3' flanking genomic polymorphic position as provided in the detailed summary of single conclains apply an individual and determining the sample from one or more polymorphic positions in a gene conclain selected from the group above; (3) constructing (M2) an individual at risk of developing a disorder conclains a protein selected from the group above; (3) constructing (M2) chaplotypes using the genes comprising grouping at least two nucleic acids acids sending tration of an ACE inhibitor and/or vasopspetidase inhibitor (c) (4) identifying (M3) an individual at risk of developing a disorder comprises one or more polymorphic positions within a gene enroding a mucleic acids sending the polymorphic data; (5) a library of nucleic acids, each of which comprising obtaining a nucleic acid sample, determining the individual comprising obtaining a nucleic acid sample, determining the composition are useful for detecting, diagnosting, treating, concleosing are useful for detecting, diagnosting, and compositions are useful for detecting, diagnosting, treating, preventing various disorders such as angioedaema and diseases which involve angiogenesis like haemangionae, tumours, sarcomas, crohn's compositions, heart failure, myocardial infarction, ventricular compositions, neath failure, myocardial infarction, ventricular compositions, neath failure, myocardial infarction, wentricular compositions, sepases in an energy and polymorphy, vascular diseases (COPP) and enterocolicies, diseases and d proteins listed above

Sequence 805 AA;

120 420 438 79 LAQMYPLQEIQNLIVKLQLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 138 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED 180 181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFERIKPLYEHLHAYVRAKLANNAYPSYISP 240 241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 300 318 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360 378 421 LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480 9 78 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVONNNAGDKWSAFLKEQST 61 LAQMYPLQEIQNLTVKLQLQALQONGSSVLSEDKSKRLNTILLNTMSTIYSTGKVCNPDNP 139 QECLLLEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSYISP 259 IGCLPAHLIGDWWGRFWTNLYSLTVPFGQKPNIDVTDAWVDQAWDAQRIFKEAEKFFVSV 319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAFLKEQST Gaps ö 100.0%; Score 3231; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0; Matches 595; Conservative Best Local Similarity 121 301 ሯ 셤 ð 셤 ò 셤 ઠે 요 δ g Š a ઠે a ò

The invention relates to an isolated nucleic acid from a human gene encoding aminopeptidase P (XPNBP2), bradykinin receptor B1 (BDKRB1), trachykinin receptor B1 (TACR1), C1 esterase inhibitor (C1NH), kallikrein (KLK1), bradykinin receptor B2 (BDKRB2), anglotensin converting enzyme 2 (ACR2) or protease inhibitor 4 (P14), comprising at least one polymorphic position. Also included are (1) a probe that hybridises to a polymorphic position as provided in the detailed summary of single nucleotide polymorphisms comprising additional 5, and 3' flanking genomic sequence; (2) analysing (M1) at least one nucleic acid sample comprising LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 498 useful DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML DPASLFHVSNDYSFIRYYTRTLYQPQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 613 New isolated nucleic acid with at least one polymorphic position, use for detecting, diagnosing and treating disorders such as angioedema, cancer, viral, bacterial or fungal infection, cardiovascular and 541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 595 559 RLGKSEPWTLALENVVGAKNMVVPPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY Zerba KE, Ma-Edmonds M, Perrone MH; Human angiotensin converting enzyme 2 variant #1. ABG77023 standard; protein; 805 AA Disclosure; Fig 37; 977pp; English (FRIM) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L. 04-DEC-2000; 2000US-0251015P. 23-JAN-2001; 2001US-0263678P. 02-MAR-2001; 2001US-0273037P. 03-DEC-2001; 2001WO-US047235 (first entry) Z, Hui L, Powell JR; 2002-619265/66. autoimmune diseases. N-PSDB; ABS60633 WO200261131-A2. rsuchihashi Z, Homo sapiens. 05-NOV-2002 08-AUG-2002. Swanson BN, ABG77023; 481 499 RESULT 8 요 ò 원

Aminopeptidase P; XPNEP2; bradykinin receptor B1; human; BDKRB1; tachykinin receptor B1; TACR1; Cl esterase inhibitor; ClNH; kallikrein 1; KLK1; bradykinin receptor B2; BDKRB2; gene therapy; and converting enzyme 2; ACB2; protease inhibitor 4; P14; angiotensin converting enzyme 2; ACB2; protease inhibitor 4; P14; polymorphism; haemangioma; tumour; sarcoma; Crohn's disease; trachoma; cardiovascular disease; angina pectoris; hypertension; heart failure; myocardial infarction; ventricular hypertrophy; vascular disease; angioedaema; anteriosclerosis; thrombosis; coronary artery disease; angioedaema; autoimmune disease; inflammatory arthritis; cancer; wound; viral infection; bacterial infection; fungal infection; COPD; chronic obstructive pulmonary disease; enterocolitis.

concaining the sample from one or more polymorphic positions in a gene encoding a protein selected from the group above; (3) constructing (M2) enployage using the genee comprising grouping at least two nucleic acids; (4) identifying (M3) an individual at risk of developing a disorder upon administration of an ACE inhibitor and/or vasopeptidase inhibitor using the polymorphic date; (5) a library of nucleic acids, each of which comprises one or more polymorphic positions within a gene encoding a human protein selected from the group above; and (6) genotyping (M4) an individual comprising obtaining a nucleic acid sample, determining the nucleotide present in at least one polymorphic position, and comparing the compositions are useful for detecting, diagnosing, treating, preventing various disorders uch as angloedame and diseases which involve anglogenesis like haemangiomas, tumours, sarcomas, Crohn's disease, trachomas, and cardiovascular diseases like angina pectoris, hypertrophy, vascular diseases, and composition, heart failure, myocardial infarction, controllar coronary artery disease, arteriosclerosis and/or atherosclerosis, and artery disease, vacunds, viral, bacterial or fungal infaction, chronic obstructive pulmonary disease (CPD) and enterocolitis (many other artification are also are also are also and arterior diseases and diseases are also and contained and arterior diseases and diseases and diseases are also are also are also and also are also and also are also are also and also are also and also are also are also are also are also and also are also are also are also are also and arterior and also are also are also are also and also are also and also are also are also are also and arterior and also are also are also are also are also and also are also and also are also are also and also are also and also are also and are also and are also and also are also and polynucleotides are also useful for chromosome identification. Antibodies against the proteins may be utilised for immunophenotyping of cell lines and biological samples. The present sequence represents a polymorphic sample from one or more individuals and determining the and biological samples. The present sequence variant of one of the proteins listed above

Sequence 805 AA;

셤 ò 셤 ò 셤 ð 셤

318 360 420 480 540 558 LAGMYPLQEIQNLTVKLQLQALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120 138 240 258 300 378 438 498 139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYBEYVVLKNEMARANHYED 198 78 79 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 379 IOYDMAYAAOPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML DPASLFHVSNDYSFIRYTRTLYQFQFQBALCQAAKHEGPLHKCDISNSTEAGQXLFNML 19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYED YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST S59 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY 613 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY 595 ö 100.0%; Score 3231; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0 Local Similarity 100. nes 595; Conservative 499 Query Match 61 121 241 301 319 421 541 181 481 Matches

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8 6

The present invention describes a new method of treating a body weight disorder, increasing muscle mass and decreasing body fat by administration of angidenenic converting enzyme (ACE) -2 modulating compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a staticularly obesity of at least grade 1, diabetes, atherosclerosis and a cation weight loss, rapid metabolism. The method is used for treating capid weight loss, rapid weight gain, anorexia, cachexia, bulimia, generalised partial lipodystrophy, familial partial lipodystrophy, concentrate metabolic rate, hyperrophy, acute heart failure, chronic heart failure, left ventricular hyperrophy, acute heart failure, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease and Huntington's disease), alzheimer's disease, parkinson's disease and Huntington's disease), myocardial infarction, cardiomyopathy, systemic inflammation response syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and

Human; anglotensin converting enzyme-2; ACB-2; body weight disorder; muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss; lipid metabolism; weight gain; anorexia; cachexia; bulima; sepsis; familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia; aberzant metabolic rate; heart failure; left ventricular hyperlipidaemia; neurodegenerative disorder; peptide hormone; cytokine processing; myocardial infarction; cardiomyopathy; inflammatory bowel disease; systemic inflammation response syndrome; polytrauma; pain; stroke; bone destruction; rheumatoid arthritis; osteoarthritis; asthma; periodontal disease; dysmenorrhoes; premature labour; prain oedema; focal injury; diffuse axonal injury; reperfusion injury; scar formation; cerebral vasospaem; subarachnoid haemorrhage; allergic disorder; adult respiratory distress syndrome; wound healing; appetite; Treating body weight disorder and increasing muscle mass comprises administering angiotensin converting enzyme-2 modulating compound. Solomon M, Stricker-Krongrad A; Human angiotensin converting enzyme-2 (ACE-2) protein. Guan B, 19. .805
/label= Mature_human_ACE_2_protein Dales NA, Example 5; Page 387-390; 395pp; English. 1. .18
/label= Signal peptide Location/Qualifiers AAU99701 standard; protein; 805 AA Gould AE, 01-NOV-2000; 2000US-00704216. 29-MAY-2001; 2001US-00870382. 19-OCT-2001; 2001US-0371741P. (MILL-) MILLENNIUM PHARM INC. 31-OCT-2001; 2001WO-US045703 (first entry Ocain TD, G Kadambi VJ, WPI; 2002-547572/58. N-PSDB; ABK87623. body mass index. WO200239997-A2. Homo sapiens 24-SEP-2002 23-MAY-2002. Acton SL, Patane M, AAU99701; Peptide Protein RESULT 10 AAU99701

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chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis and periodontal disease, dysmenorrhoea, premature labour, brain oedema following focal injury, diffuse axonal injury, stroke, reperfusion injury, cerebral vasospasm after subarachnoid haemorrhage, allergic disorders including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, increases muscle mass and decreases body fat of subject having body mass index of greater than 23 (preferably 24.9)kg/m²2. The present amino acid sequence represents the human ACE-2 protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
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                                                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                                                                                                                                    QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEBYVVLKNEMARANHYED 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEWARANHYED 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 IGCLPAHLIGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
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                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                                                                                                                                                                                                                       19 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTISTIXSTGKVCNPDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPNMTQGFWENSMLIDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 IQYDMAYAAQPFLLKNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKOALTIVGTLPFTYMLEKWRWVPKGEIPKDOMMKKWWEMKREIVGVVEPVPHDETYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 DPASLFHVSNDYSFIRXYTRTLYQPQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                                                                                                                                                                                                                                                          1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFRPLFTWLKDONKNSFVGWSTDWSPY 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 RIGKSEPWILALENVVGAKNMAVRPLLANYFEPLFTWIKDQNKNSFVGWSTDWSPY 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; enzyme; Zace2; zinc metallopeptidase; ulcerative colitis; inflammation; inflammatory bowel disease; arthritis; enterocolitis; Crohn's disease; gene therapy; transgenic.
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0
                                                                                                                                                                                                                    100.0%; Score 3231; DB 5; Length 805; 100.0%; Pred. No. 6.1e-288;
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                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU07731 standard; protein; 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 595; Conservative
                                                                                                                                                                                  Sequence 805 AA;
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The invention relates to an isolated polypeptide, comprising fully defined human Zace2, murine Zace-5, or murine Zace2-10 polypeptide. An expression vector containing Zace2 pormucleotide is useful for producing Zace2 protein. The polymucleotide is useful as a diagnostic probe for detecting a product of Zace2 gene expression in a biological sample. The polypeptide is also useful for decreasing inflammation associated with a condition such as inflammatory bowel disease, arthritis or enterocolitis. The polypeptide is useful for treating Crohn's disease and ulcerative colitis. The polypeptide is useful for producing labelled angiotensin II, for identifying modulators of Zinc protease activity and for identifying angiotensin converting enzyme (ACB) inhibitors. The polymucleotide is useful in gene therapy techniques to treat the above mentioned disorders. The polymucleotide is also useful for determining whether a subject's chromosome contains a mutation in the Zace2 gene. The present sequence represents the amino acid sequence of human zinc metallopeptidase Zace2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEBYVVLKWEMARANHYED 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated human or murine Zace2 polypeptide useful for reducing inflammation in conditions such as inflammatory bowel disease, arthritis, enterocolitis, ulcerative colitis and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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/label= Expanded_zinc_binding_region
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100.0%; Pred. No. 6.1e-288;
iive 0; Mismatches 0;
                                                                                                   /label= Transmembrane domain
                                            374. 378
/label= Zinc-binding_motif
739. 761
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location/Qualifiers
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                                                                                                                                                                                                                                            13-MAY-1999; 99US-0133952P.
27-AUG-1999; 99US-0151181P.
03-MAY-2000; 2000US-00563516.
                                                                                                                                                                                                           16-OCT-2001; 2001US-00978385.
                                                                                                                                                                                                                                                                                                                                                      Piddington CS, Petrie C,
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Best Local Similarity 100.
Matches 595; Conservative
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                 319 GLPNWTQGFWENSMLTDPGNVQXAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                       LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
                                                                                                                                        LLKQALTIVGTLPFTYMLEKWRWNVFKGBIPKDQWMKKWWEMKRBIVGVVEPVPHDETYC
GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                                                                                                                                   DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
                                                                                                                                                                                                     499 DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHGGPLHKCDISNSTEAGQKLFNML
                                                            1QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                       379 IQYDMAYAAQPPLLENGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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ADA03344 standard; protein; 805 AA RESULT 12 ADA0334

ADA03344;

(first entry) 06-NOV-2003

Human angiotensin converting enzyme 2-like protein.

whypotensive; cardiant; cerebroprotective; antiatherosclerotic; analgesic; antinflammatory; nephrotropic; hypertensive; vasotropic; cytostatic; antinflammatory; nephrotropic; neuroprotective; antiparkinacinan; nootropic; antirheumatic; antiathritic; antiparkinacinan; antidautic; antiathritic; antigout; tranquillizer; valunerary; antidabetic; dermatological; immunosuppressive; hepatotropic; antipacterial; angiotensin converting enzyme; ACB-2; antipacterial; angiotensin converting enzyme; ACB-2; wangiotensin converting enzyme; ACB-2; wangiotensin converting enzyme; ACB-2; wasoconstriction; epitope; left ventricular failure; atherosclerotic heart disease; stenosis; pain; inflammatory reaction; whistenine; vasoconstriction; epitope; aldosterone; cell proliferation; renal disorder; acute glomerulonephritis; immunophenotyping; cardiac myocyte; Bowman's capsule; hypotensin; ischemia; asthma; allergy; wardiac myocyte; Bowman's capsule; hypotensin; ischemia; asthma; allergy; wheumatoid arthritis; gout; trauma; dermatitis; diabetes mellitus; sjout; AlbS; sepsis.

Homo sapiens

WO200298448-A1

03-JUN-2002; 2002WO-US017199.

04-JUN-2001; 2001US-0294976P

(HUMA-) HUMAN GENOME SCI INC

8 Wescott Huang L, Sanyal I, Albert VR, Rosen CA, Parry TJ, Sekut L;

WPI; 2003-140552/13. N-PSDB; ADA03343 Novel angiotensin converting enzyme-2 binding polypeptide useful for treating, preventing or ameliorating hypertension, congestive heart failure, stroke, left ventricular failure and atherosclerotic heart disease. Novel

558

499

Disclosure; Page 239-241; 246pp; English

The invention relates to novel isolated angiotensin converting enzyme (ACE)-2 binding polypeptides (I), which are useful for treating, preventing or ameliorating Mypertension, congestive heart disease in an animal. The peptides are useful for detecting, isolating, or purifying CC ACE-2 proteins or ACE-2 like polypeptides in solutions, mixtures, or biological samples; for inhibiting or reducing stenosis, pain, cinflammatory reactions, abnormal histamine release, vasoconstriction, diseases or disorders related to vasoconstriction, and diseases and/or disorders associated with aberrant action of ACE-2; to detect, isolate, or remove ACE-2 target proteins in solutions, and also to identify cor remove ACE-2; to detect, diagnose, prognose, or monitor cardiovascular diseases, and disorders associated with aberrant calculations, and disorders especially or cell proliferation; for preventing and treating candisorders, e.g., acute glomerulonephritis, and diseases associated with aberrant calculations or assay protein levels in a biological samples by their ACE-2 expression, and for identifying cells, such as cardiac myocytes, endothelial and epithelial cells of Bowman's capsule. The peptides are especially useful for treating, preventing, or ameliorating diseases or disorders associated with hypotensin, isochemia, asthma, allergy, multiple sclerosis, cancers, Parkinson's and Alzheimer's diseases, rheumatoid active hepatitis, Crohn's disease, cardiaces, AIDS, and sepsis. In an example of the invention, ACE-2 cardiaces. AIDS, and sepsis. In an example of the invention, decises of peptide families. This sequence represents a human angiotensin converting curyme 2-like protein. ¥8888888888888888888888888888888888

Sequence 805 AA;

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ö 540 480 438 9 78 139 QECLILEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVIKNEMARANHYED LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC STIEEQAKTFLDKENHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAFLKEQST LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRINTILNTMSTIYSTGKVCNPDNP YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 421 LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP QECLLLEPGLINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML Gaps ö 100.0%; Score 3231; DB 6; Length 805; 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 595; Conservative н 19 61 199 241 301 361 439 Query Match 79 121 181 481

198

QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVULKNEMARANHYED

QECLILEPGINEIMANSIDYNERLWAWESWRSEVGKQIRPLYEEYVVIKNEMARANHYED

258 300

IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKBAEKFFVSV

360

GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFR1LMCTKVTMDDFLTAHHEMGH

420 438

IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF

480

540 558

DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML

RIGKSEPWTLALENVVGAKNMVKPLLINYFEPLFTWLKDQNKNSFVGWSTDWSPY

LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKREIVGVVBPVPHDETYC

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259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV 318
                                                                                                                                                                                                                                                                   319 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 378
                                                                                                                181 YGDYWRGDYEVNGYDGYDYSRGQLIBDYEHTFEBIKPLYEHLHAYVRAKLMNAYPSYISP
                                                                                                                                     199 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for increasing vasoconstriction or ameliorating a disorder resulting from low blood pressure, which comprises administering to an individual an amount of angiotensin II in compination with angiotensin 1-9. Angiotensin has hypertensive and compination with angiotensin 1-9. Angiotensin has hypertensive and compination with angiotensin or ameliorating a disorder resulting from IOV increasing vasoconstriction or ameliorating a disorder resulting from IOV blood pressure, such as hypotension, shock or syncope. ABR5553 to ABR55708 represent angiotensin converting enzyme 2 (ACE-2) binding peptides, ABR56709 to ABR5672 and ACC79021 to ACC79025 represent sequences used in the exemplification of the present invention. Human ACE 2 is located to chromosome X, more specifically to Xp22. N.B. ABR5653 to ABR56572 represent SRQ ID NO:1 to 10 and should be the same as ABR56572 represent SRQ ID NO:1 to 10 and should be the same as ABR56573 to ABR56582 but the Z's given at the beginning and end of the peptides in the disclosure have been expanded to Glx in the Sequence Listing and in this case the Z's do not represent Gln or Glu (see pages 1 to 7): SRQ ID NO:40 to 136 in the Sequence Listing (see also pages 7 to 17) to 177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing vasoconstriction or ameliorating a disorder resulting from low blood pressure, e.g. hypotension, shock or syncope, comprises administering an angiotensin II in combination with angiotensin 1-9 to an individual.
                                  613
                                                                                                                                                                                                                                              Human, angiotensin converting enzyme 2, ACE-2 binding, ACE-2;
vasoconstriction; low blood pressure; angiotensin II; angiotensin,
hypertensive; vasotropic; vaccine; hypotension; shock; syncope.
Length 805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 3231; DB 6;
100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 227-229; 237pp; English.
                                                                                                                                                                                                                 Human ACE-2 protein SEQ ID NO:142.
                                                                                                                  ABR56712 standard; protein; 805
                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2002; 2002WO-US017213
                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-JUN-2001; 2001US-0295004P
                                                                                                                                                                                (first entry)
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                                                                                                                                                 ABR56712;
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Identification of compound that modulates bioactivity of angiotensin converting enzymes-2 polypeptide, by detecting modulation of the bioactivity of polypeptide that is contacted with test compound as compared to control.
                                                                                   angiotensin converting enzyme-2; ACE-2; human; enzyme;
                                                              Human angiotensin converting enzyme-2 (ACE-2).
                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID NO 2; 91pp; English
ADL95395 standard; protein; 805 AA
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                                                                                                                                                                                                  97US-00989299.
                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                              99US-00407427
                                                                                                                                                                                                                                                                         WPI; 2003-895335/82.
N-PSDB; ADL95394, ADL95396.
                                         (first entry)
                                                                                                                                                                                                                                                      Robison KE,
                                                                                 bioactivity; ang:
carboxypeptidase
                                                                                                                  Homo sapiens.
                                                                                                                                     US6610497-B1
                                                                                                                                                                              29-SEP-1999;
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                                         20-MAY-2004
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                    ADL95395;
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Gaps

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Best Local Similarity 100. Matches 595; Conservative

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9 78 61 LAQMYPLQEIQNLTVXLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120

STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST 1 STIEBQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST

Human angiotensin converting enzyme-2 (ACE-2) N720D

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The invention describes a compound that modulates bioactivity of an anglotensin converting enzyme-2 (ACE-2) polypeptide. The compound is identified by contacting an ACE-2 polypeptide with a test compound under conditions for modulation of the bioactivity of the polypeptide; and detecting modulation of the bioactivity of the polypeptide by the test compound as compared to a control. Also described is a method for modulating the bioactivity of an ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-2 polypeptide by contacting the ACE-3 polypeptide with a compound that has been identified. The method is useful for identifying a compound that modulates the bioactivity of angiorensin converting enzyme-2 peptides. The inventive method identifies other potential substrates of ACE-2 polypeptides and the product of the enzymatic reaction. The comparison of the mass spectra of the test compound was converted into a new compound, in which case the test compound is a substrate of the ACE-2 polypeptide. This is the amino acid sequence of human angiotensin converting enzyme-2 (ACE-2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAWVDQAWDAQRIFKEAEKFVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
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Matches 595; Conservative
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The invention describes a compound that modulates bioactivity of an angiotensin converting enzyme-2 (ACB-2) polypeptide. The compound is dentified by contacting an ACB-2 polypeptide with a test compound under conditions for modulation of the bioactivity of the polypeptide; and detecting modulation of the bioactivity of the polypeptide by the test compound as compared to a control. Also described is a method for modulating the bioactivity of an ACB-2 polypeptide by contacting the ACB-2 polypeptide by contacting the ACB-2 polypeptide by contacting the ACB-3 polypeptide with a compound that has been identified. The method is cusful for identifying a compound that modulates the bioactivity of an ACB-3 polypeptides and the product of the angiotensin converting enzyme-2 peptides. The inventive method identifies other potential substrates of ACB-2 polypeptides and the product of the compound with that of the reaction mixture after incubation indicates whether the test compound is a substrate of the ACB-2 polypeptide. This is the amino acid sequence of human angiotensin converting enzyme-2 (ACB-2) (N72DD mutcant. Note: This sequence does not appear in the printed converting enzyme-1 (ACB-2) entotication but has been created by the indexer using information given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of compound that modulates bioactivity of angiotensin converting enzymes-2 polypeptide, by detecting modulation of the bioactivity of polypeptide that is contacted with test compound as
                                  bioactivity; angiotensin converting enzyme-2; ACE-2; human; enzyme;
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100.0%; Pred. No. 6.1e-288;
ive 0; Mismatches 0;
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                                                                                                                                             Location/Qualifiers
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98US-00163648.
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Matches 595; Conservative
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                                                                                         Homo sapiens
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ADL95494 standard; protein; 805

20-MAY-2004 (first entry)

ADL95494;

RESULT 15
ADL95494
ID ADL95X
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GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
                                                                                              IQYDMAYAAQPFLLRNGANEGFHRAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
                               IGCLPAHLLGDWWGRFWTNLYSLTVPFGQRPNIDVTDAMVDQAWDAQRIFKBEKFFVSV 300
                                                                                                                            LLKQALTIVGTLPFTYMLEKWRWNVPKGEIPKDQMMKKWWEMKREIVGVVBPVPHDETYC 480
                                                                                                                                                            DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHGGPLHKCDISNSTEAGQKLFNML 540
YGDYWRGDYEVNGVDCYDYSRGQLIEDVEHTPEBIKPLYEHLHAYVRAKLMNAYPSYISP 240
                                                                                                                                                                                           RIGKSEPWTLALENVVGAKAMAVRPLLNYFEPLFTWLKDQNKNSFVGMSTDMSPY 595
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Search completed: March 28, 2006, 11:09:51 Job time : 137.885 secs THIS PAGE BLANK (USPTO)

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- 2006 Biocceleration Ltd.
GenCore (c) 1993
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(without alignments)
2618.576 Million cell updates/sec 2006, 11:10:19 28, March Run on:

US-10-659-000-4 3231 1 STIEEQAKTFLDKFNHEAED......WLKDQNKNSFVGWSTDWSPY 595 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	hypothetical prote	peptidyl-dipeptida	angiotensin-conver	peptidyl-dipeptida	hypothetical prote			probable thermosta	peptide synthetase	zinc metalloprotei	zinc metalloprotei	carboxypeptidase h	probable thermosta	oligoendopeptidase	beta-galactosidase	1,4-alpha-glucan b	G-utrophin - mouse	probable oligoendo	oligopeptidase A -	TRAP-like protein	probable glycosyl								
SUMMARIES	ΩI	T14762	S05238	A31759	A35655	A34171	JC2038	JC2489	A34402	835484	S65472	JC5374	A57533	T15792	C83696	AF1310	AE1682	AI2011	B82938	D82881	D69943	B72561	AB3511	T30574	S40048	I48373	A75573	F75370	8	AI0968
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	Score	3231	1335	1335	1334	1334	1310	1307	1281	1281	1054.5	1027.5	1022	635.5	157	154	147	139.5	139	136	135	124	121	121	118	117.5	115.5	-	113.5	113
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thermostable carbo protein containing	cytoplasmic dynein	probable carboxype	beta-galactosidase	NMDA receptor-bind	1,4-alpha-glucan b	lantibiotic epider	probable SNF2 subf	utrophin - human	1,4-alpha-glucan b	hypothetical prote	hypothetical prote	•~	hypothetical helic	outer layer protei
B82202 H97226	T30838	AG0281	T30551	T08880	E98000	823416	A84683	828381	G95129	AG2285	T29486	T51292	T39568	VPXRPC
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111.5	110.5	110	110	110	109.5	109	108.5	108.5	107.5	107.5	107.5	107.5	107.5	107
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ALIGNMENTS

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Gaps ö 0; Indels Best Local Similarity 100.0%; Pred. No. 3.6e-224; Matches 595; Conservative 0; Mismatches 0;

STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST

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120 137 11 LAQMYPLQBIQNLTVKLQLQALQQNGSSVLSEDXSKRLNTILNTMSTIYSTGKVCNPDNP 18 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNWNNAGDKWSAFLKEQST 61 셤 ò 셤

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480 437 LLKQALTIVGTLPFTYMLEKWRWVPKGEIPKDQWMKKWWEMKRIVGVVEPVPHDETYC 378 421 셤 ઠ

Db 438 LLKQALTIVGTLPFTYMLEKWRWNFKGEIPKDQMMKKWWEMKRRIVGVVEPVPHDETYC 497 QY 481 DPASLPHVSNDYSFIRYYTRTLYQFQFQALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540	Db 290 YGAQHINLEGPIPAHLLGNWMAQTWSNIYDLVVPFPSAPSMDTTEAMLKQGWTPRRMFKE 349 Qy 293 AEKFFVSVGLPNWTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
RESULT 2 S05238 Species: Anone sapiens A (EC 3.4.15.1) precursor, testicular splice form - human NyAlternate names: angiotensin I-converting enzyme (ACE); CD143; dipeptidyl carboxypepti C;Species: Homo sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004 C;Accession: S05238, A3399- R;Lattion, A.L.; Soubrier, F.; Allegrini, J.; Hubert, C.; Corvol, P.; Alhenc-Gelas, F. FEBS Lett. 252, 99-104, 1989 A;Ritle: The testicular transcript of the angiotensin I-converting enzyme encodes for th A;Recession: S05238 A;Rocession: S05238 A	
A; Reference number: A33979; MUID: 90046671; PMID: 2554286 A; Accession: A33979 A; Molecule type: mRNA A; Residues: 1-732 < EHL.> A; Experimental source: clones R1.2 and T8B A; Note: neither the complete nucleic acid sequence nor the complete translation are show C; Comment: For the renal and pulmonary splice form, see PIR: A31759. C; Genetics: A; Gene: GDB: DCP1; ACE A; Cross-references: GDB: DCP1; ACE A; Cross-references: GDB: 119840; OMIM: 106180	A31759
C.Function: A, Description: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptides A, Description: mammalian peptidyl-dipeptidase A. C.Superfamily: mammalian peptidyl-dipeptidase A. C.Superfamily: mammalian peptidyl-dipeptidase A. C.Superfamily: mathematics signal sequence #status predicted <515. F.12.1/Domain: signal sequence #status predicted <815. F.22.732/Product: peptidyl dipeptidase I #status predicted <arm> F.103.121.140,186,388,617.551/Binding site: carbohydrate (Asn) (covalent) #status predicted <f415 #status="" (his,="" 1335;="" 1;="" 41.3%;="" 732;<="" active="" best="" db="" f.415="" glu="" glu)="" his,="" length="" local="" match="" predicted="" query="" score="" similarity="" site:="" td=""><td>A; Residues: 1-1306 <sous 1-1306="" 106,="" 1989="" 2558109="" 442-445,="" 90110025;="" <sous="" a;="" accession:="" amino="" angiotensin-converting="" biochem:="" by="" cross-references:="" deter="" drotein="" end="" enzyme="" experimental="" f="" f.;="" gb:j04144;="" h.="" high-performance="" human="" including="" j.="" k.;="" kidney="" lic="" lung="" lung<="" mature="" molecule="" muid:="" n.;="" nid:g178285;="" note:="" number:="" of="" ohishi,="" p12821;="" parts="" pidn:="" pmid:="" pq0004="" pq0004;="" protein="" protein,="" purification="" r;="" reference="" residues:="" sequence,="" seyama,="" shimitau,="" source:="" t.;="" takaku,="" taxteuchi,="" td="" the="" this="" title:="" type:="" uniparc:="" uniprot:="" upi000002b8ad;="" upi0000172a3d="" were="" y.;="" yotsumoto,=""></sous></td></f415></arm>	A; Residues: 1-1306 <sous 1-1306="" 106,="" 1989="" 2558109="" 442-445,="" 90110025;="" <sous="" a;="" accession:="" amino="" angiotensin-converting="" biochem:="" by="" cross-references:="" deter="" drotein="" end="" enzyme="" experimental="" f="" f.;="" gb:j04144;="" h.="" high-performance="" human="" including="" j.="" k.;="" kidney="" lic="" lung="" lung<="" mature="" molecule="" muid:="" n.;="" nid:g178285;="" note:="" number:="" of="" ohishi,="" p12821;="" parts="" pidn:="" pmid:="" pq0004="" pq0004;="" protein="" protein,="" purification="" r;="" reference="" residues:="" sequence,="" seyama,="" shimitau,="" source:="" t.;="" takaku,="" taxteuchi,="" td="" the="" this="" title:="" type:="" uniparc:="" uniprot:="" upi000002b8ad;="" upi0000172a3d="" were="" y.;="" yotsumoto,=""></sous>
## 202; Indel## 34; Gaps 9; TNITEENVONMNNAGDKWSA 53	C; Comment: This splice form is found in many tissues, in particular kidney and lung vasci C; Comment: This splice form is found in many tissues, in particular kidney and lung vasci C; Genetics: GDB:DCP1; ACE A; Gene: GDB:DCP1; ACE A; Gene: GDB:DCP1; ACE A; May position: 17q23-17q23 C; Function: A; Map position: catalyzes the hydrolysis of dipeptides from the carboxyl end of polypeptic C; Function: A; Note: plays a role in the control of blood pressure by catalyzing the conversion of ang C; Superfamily: mammalian peptidyl-dipeptidase A C; Superfamily: mammalian peptidyl-dipeptidase A C; Keywords: alternative splicing; blood pressure control; glycoprotein; kidney; lung; met F; 1-29/Domain: signal sequence #status predicted <sig>F; 30-1366/Product: peptidyl dipeptidase I #status predicted <trm>F; 30-1306/Product: peptidyl dipeptidase I #status predicted <trm>F; 30-1306/Domain: transmembrane #status predicted <trm>F; 300,394 Bainding site: zinc, (His) #status predicted F; 380,394 Bainding site: zinc, catalytic (His, His, Glu) #status predicted F; 989,922,1008/Binding site: zinc, catalytic (His, His, Glu) #status predicted F; 989/Active site: Glu #status predicted C; Core 1335; DB 1; Length 1306;</trm></trm></trm></sig>

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Addityl-dipeptidase A (EC 3.4.15.1) precursor - mouse
Nohlterate names ACE; anajotenshan-converting enzyme; carboxycathepsin; dipeptidyl carbo
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus anasculus (house mouse)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Species: Musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Musculus (house mouse)
A.Fiberintein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, E.A.
A.Reference number: A34171; MUID:89308599; PMID:2545691
A.Fitle: Mouse angiotensin-converting enzyme is a protein composed of two homologous dome A; Residues: 1-1312 - GERS.
A.Focasion: A.Species: Mulpon:POP470; UNIPARC:UP10000029FEE; GB:J04947
A.Reference number: A29210
A.Fitle: The isolation of angiotensin-converting enzyme cDNA.
A.Reference number: A29220; MUID:88298730; PMID:2841312
A.Accession: A29220
A.MUID:88298730; PMID:2841312
A.Accession: A29220
A.MUID:88298730; PMID:2841312
A.Accession: A29220
A.MUID:88215372; PMID:283538
A.FITLE: Partial protein sequence of mouse and bovine kidney angiotensin converting enzym A.Residues: 35-54 - GES;
A.Accession: A61477
A.Accession: A61474
A.Accessi
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kedeuse: 1-732 <HOW>
A;Cross-references: UNIPROT:P22967; UNIPARC:UPI0000120BD5; GB:M55333; NID:g191589; PIDN:
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; zi
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NyAlternate names: peptidyl-dipeptidase I, testis
Cispecias: Mus musculus (house mouse)
Cispecias: Mus musculus (house mouse)
Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CiAccession: A35655
RiHoward, T.E.; Shai, S.Y.; Langford, K.G.; Martin, B.M.; Bernstein, K.E.
Mol. Cell. Biol. 10, 4294-4302, 1990
A;Title: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated A;Reference number: A35655; MUID:90318396; PMID:2164636
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                                                                                                                                                                                          54 PLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGK
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                                                                                                                                        2 TIBEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE-----NVQNMNNAGDKWSA
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41.3%; Score 1334; DB 1; Length 732;
Best Local Similarity 42.6%; Pred. No. 7.8e-88;
Matches 255; Conservative 112; Mismatches 213; Indels 18;
                                                 34;
                                                 Indels
Local Similarity 41.9%; Pred. No. 1.6e-87; hes 254; Conservative 116; Mismatches 202;
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NiAlternate names: angiotensin converting enzyme; kininase II
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JU2038
R;Koike, G.; Krieger, J.E.; Jacob, H.J.; Mukoyama, M.; Pratt, R.E.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 198, 380-386, 1994
A;Title: Angiotensin converting enzyme and genetic hypertension: Cloning of rat cDNAs and A;Reference number: JU2038
A;Accession: JU2038
A;Accession: JU2038
A;Accession: JU2038
A;Molecule type: mRNA
A;Residues: 1-1131 a.KOI>
A;Cross-references: UNIPROT:P47820; UNIPARC:UP1000016828P; GB:U03734; NID:g437289; PIDN: A;Cross-references: UNIPROT:P47820; UNIPARC:UP1000016828P; GB:U03734; NID:g437289; PIDN: C;Comment: This enzyme is a zinc-containg dicarboxy peptidase that cleaves angiotensin I C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the ta C;Comment: This enzyme plays a critical role in blood pressure homeostasis and is the c;Comment: This enzyme la a zinc-containg dicarboxy peptidase that Cleaves angiotensin I C;Comment: This enzyme la peptidy1-dipeptidase A
C;Comment: This enzyme la peptidy1-dipeptide hydrolase; transmembrane protein; zi F;333-400,990-998/Region: catalytic #status predicted <TWM>
F;325-400-998/Region: catalytic #status predicted <TWM>
C;Keywords: alternative splicing; blood pressure control; membrane protein; peptidyldipe
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>
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                                                                                                                                           Length 1312;
                                                                                                                                        Query Match
41.3%; Score 1334; DB 1; Length 13:
Best Local Similarity 42.6%; Pred. No. 1.9e-87;
Matches 255; Conservative 112; Mismatches 213; Indels
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DB 1; Length 1313;

40.5%; Score 1310;

Query Match

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Deptidy1-dipeptidase A (EC 3.4.15.1) - chicken
NyAlternate names: anglotensin converting enzyme
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: JC2489
B;Catcession: JC2489
B;Catcession: JC2489
A;Title: Chicken lacks the testis specific isozyme of anglotensin converting enzyme founc
A;Reference number: JC2489
A;Title: Chicken lacks the testis specific isozyme of anglotensin converting enzyme founc
A;Reference number: JC2489
A;Rocession: JC2489
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A;Rocession: JC2489
A;Rocession: JC3489
A;Rocessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       768 TCLSLEPDLTNIMATSRKYEELLWVWKSWRDKVGRAILPFFPKYVDFSNKIAKLNGYSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPNMTQGFWENSMLTDPGNVQXAVCHPTAWDLGKG-DFRILMCTKVTMDDFLTAHHEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            938 GLLPVPPEFWNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMG
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                                                                                                                                                                                                                                                                                                                                      ECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKOLRPLYEEYVVLKNEMARANHYEDY
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                                                  Gaps
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                                              18;
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    Pred. No. 1e-85;
5; Mismatches 214; Indels
                                          251; Conservative 115;
        42.08;
Best Local Similarity
Matches 251; Conserv
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A,Accession: C18700
A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Rosidues: 33-35,'SN',38-39,'SS';'FAEL',737 <IWA>
A,Rosidues: 33-35,'SN',38-39,'SS';'FAEL',737 <IWA>
A,Cross-references: UNIPARC:UP10000172A42; UNIPARC:UP10000172A43
A,Cross-references: UNIPARC:UP10000172A42; UNIPARC:UP10000172A43
A,Note: several of the amino acids in reported are tentative
C,Comment: The pulmonary and testicular isoforms of this enzyme differ substantially in typests that the two isoforms arise by alternative splicing of one gene.
C,Superfamily: mammalian peptidyl-dipeptidase A
C,Superfamily: mammalian peptidyl-dipeptidase A
C,Keywords: alternative splicing; peptidyldipeptide hydrolase; testis; transmembrane prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 NAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIF 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHYGAQHINLEGPIPAHLLGNWWAQTWSNIYDLVAPFPSASTWDATEAMIKQGWTPRRMF
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                                                                                                                                                                                                                                                                                                                              Query Match 39.6%; Score 1281; DB 1; Length 737; Best Local Similarity 41.0%; Pred. No. 5.1e-84; Matches 249; Conservative 110; Mismatches 211; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIBEGAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEB-----NVQNMNN--AGDKW
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A; Molecule type: mRNA
A; Residues: 1-1309 < THE>
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N.Alternate names: angiotensin I-converting enzyme; dipeptidyl carboxypeptidase I; peptid C. Species Orycolagus cuniculus (domestic rabbit)

C. Species Orycolagus cuniculus (domestic rabbit)

C. Species Orycolagus cuniculus (domestic rabbit)

C. Accession: A34402; A60724; A36232; C18700

R. Kumar, R. S.; Kusari, J.; Roy, N. N.; Soffer, R.L.; Sen, G.C.

J. Biol. Chem. 264, 16754, 1989

A; Reference number: A34402; MUID:89380303; PMID:2550457

A; Reference number: A34402; MUID:89380303; PMID:2550457

A; Residues: 1-737 <KUM-A

A; Residues: 1-737
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A; Residues: 154-160; 236-242 < CHE>
A; Residues: 154-160; 236-242 < CHE>
A; Crose-references: UNIPARC: UPI0000172A40; UNIPARC: UPI0000172A41
R; Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A; Title: The NH2-and COOH-terminal sequences of the angiotensin-converting enzyme isozym
A; Reference number: A90107; MUID:83048249; PMID:6291514
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                                                                                                      QECLILLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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604 QFDPSDFQDETVTRILNXCLSVLBRAALPEDELKEYNTLLSDMETTYSVAKVCRENNTFHP
                                                                                                                                                                                                                                                                           119 NGAYWRSLYETPTFE------BDLERLYLQLOPLYLNLHAYVRRALYNKYGAEHIS
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                                                                                                                                                                                                                                                                                                                                                                       PIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVS
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peptidyl-dipeptidase A (BC 3.4.15.1) precursor - horn fly
Nalernate names: anglotensin I-converting enzyme
C;Species Haematobia Irritans (horn fly)
R;Wijffelb, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, P. Bur. J. Blochem. 237, 414-423, 1996
A;Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran A;Reference number: 865431; MUID:96215437; PMID:8647080
A;Accession: 865472
A;Molecule type: DABA
A;Residues: 1-611 (WIJ)
A;Cross-references: UNIPROT:010715; UNIPARC:UPI0000125220; EMBL:L43965; NID:g908759; PIDN
A;Accession: 865431
A;Acces
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   865 RHYGAQHINLEGPIPAHLLGNWWAQTWSNIYDLVAPFPSASTWDATEAMIKQGWTPRRMF 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAKCDLSLDPEIEEIITKSRDPEELKYYWTQFYDKAGTPTRSNFEKYVELNTKSAKLNNF
                                                                                                         DFLTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 470 VEPVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 TEAGQKLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQN--KNSFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 STIEEQAKT-FLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 TLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDYGDYWRGDYEVNGVDGYDYSRGQLIED-VEHTFEBIKPLYEHLHAYVRAKLMNAY-PS
                                                                       KEAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMD
                                                                                                                                                                                                                                                                                                                                   410 FQEDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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al Similarity 37.7%; Pred. No. 7.4e-68;
222; Conservative 105; Mismatches 239; Indels
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                                                                                                                                                                                                                                                                             R. Jawata, R. J. Lai, C.Y.; El-Dorry, H.A.; Soffer, R.L.
Biochem. Biophys. Res. Commun. 107, 1097-1103, 1982
A.Title: The NHZ-and COCH-terminal sequences of the angiotensin-converting enzyme isozyme A. Reference number: A90107; MUID:83048249; PMID:6291514
A.Accession: A18700
A.Title: The winkara, T.J.; Sen, G.C.
J. Blol. Chem. 266, 3844-3862, 1991
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A.Accession: A49726; MUID:91124568; PMID:8294466
A.Accession: A497266; MUID:94124568; PMID:8294466
A.Accession: A497266
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Biochem. J. 278, 375-380, 1991
A;Title: The Mg(2+)-ATPase of rabbit skeletal-muscle transverse tubule is a highly glycc
A;Reference number: 817509, MUID:91378880; PMID:1654880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Comment: This enzyme converts angiotensin I to angiotensin II in presence of divalent ver, the enzyme has been found also in renal tubules and intestinal mucosa. C; Keywords: alternative splicing; blood presence control; chloride; glycoprotein; intess F;1-33/Domain: signal sequence #status predicted <SIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :34-1309/Product: peptidyl-dipeptidase A, pulmonary #status experimental <MAT>
:59,79,150,322,448,512,680,698,717,945,1194/Binding site: carbohydrate (Asn) (covalent)
UNIPROT: Q9TRW7; UNIPARC: UPI0000172A44; EMBL: X62551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAY-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 SAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYST 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ARRFDVSNFQNATSKRIIKKVQDLQRAVLPVKELEEYNQILLDMETIYSV 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GKVCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEE------NVQNMNN--AGDKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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                                  R;Iwata, K.; Blacher, R.; Soffer, R.L.; Lai, C.Y.
Arch. Biochem. Biophys. 227, 188-201, 1983
A;Reference number: A23455; MUID:84051289; PMID:6314908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.6%; Score 1281; DB 1;
41.0%; Pred. No. 1.2e-83;
tive 110; Mismatches 211;
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A;Residues: 34-47,'N', 49-55 < IWA>
A;Cross-references: UNIPARC:UP1000172A45
A;Experimental source: lung
R;Iwata, K.; Lai, C.Y.; El-Dorry, H.A.; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule_type: protein
A;Residues: 34-55 <KIR>
A;Cross-references: UNIPARC:UP100000870D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: protein
Residues: 1236-1258 <RAM>
Cross-references: UNIPARC:UPI0000172A49
      Cross-references: UNIPROT: P12822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S17509
A;Status: preliminary
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es 249;
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237 YISPIGCLPAHLLGDWMGRFWTNLYSLTVPFGQKDNIDVTDAMVDQAWDAQRIFKEAEKF :	382 YYLQYEQQPAVYRGAPNPGPHEAVGDVIALSVMSAKHLKAIGLIE-NGRLDEKSRINQLF
247 VVSKTGPLPMHLLGNMWAQQWSSIADIVSPFPEKPLVDVSDEMVAQGYTPLKMFQMGDDF	423 KQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQMMKKWWEMKREIVGVVEPVPHDETYCDP
QY 297 FVSVGLPUNTQGFWENSMLTDPGNVQKAVCHPTAWDLG-KGDFRILMCTKVTWDDFLTAH 355	Db 441 KQALSKIVFLPFGYAVDKYRYAVFRNELDESQWNCGFWQNRSEFGGVBPPVFRTEKDFDP 500 Qy 483 ASLFHVSNDXSFIRYYTRTLYQFQFQBALCQAAKHEGPLHKCDISNSTEAGQKL 536
Qy 356 HEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNE 415	501
Db 367 HEMGHIQYFLQYQHQPFVYRTGANPGFHEAVGDVLSLSVSTPKHLERVGLLK-NYVSDNE 425	Qy 537 FNMLRLGKSEPWTLALENVVGAKNMVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSP 594
QY 416 TEINFLLKQALTIVGTLPFTYMLEKNRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPH 475	Db 561 SQFLSKGNSRHWKBVLEBFTGETEMDPAALLEYFEPLYQWLKQENSRLGVPLGWGP 616
OY 476 DETYCDPASLPHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNS 529	RESULT 12 A57533 Poptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila melanogaster) N;Alternate names: angiotensin-converting enzyme
OY 530 TEAGOXLENMIRIGKSEPWTLALENVVGAKAMNVRPLLNYFBPLFTWLK 578	C;Species: Drosophila melanogaster C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 26-Feb-1998 C;Accession: A57533 R;Cornell, M.J.; Williams, T.A.; Lamango, N.S.; Coates, D.; Corvol, P.; Soubrier, F.; Ho
RESULT 11 JC5374	J. Biol. Chem. 270, 13613-13619, 1995 A,Title: Cloning and expression of an evolutionary conserved single-domain angiotensin cc A,Reference number: A57533; MUID:95293950; PMID:7775412 A,Accession: A57533
angiotensin-converting enzyme-related protein - fruit fly (Drosophila melanogaster) C:Species: Drosophila melanogaster C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004 C:Accession: JC5374	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-615 < COR> A; Cross-references: UNIPARC: UPI0000175887; GB: U25344
RiTaylor, C.A.M.; Coates, D.; Shirras, A.D. Gene 181, 191-197, 1996 A.Title: The Acer gene of Drosophila codes for an angiotensin-converting enzyme homologual A. Reference number: JC5374; MUID:97128790; PMID:8973330	
A;MOJECTLE type: mRNA A;MOJECTLE type: mRNA A;Residues: 1-630 <tax> A;Cross-references: UNIPROT:Q24222; UNIPARC:UPI0000075442; EMBL:X96913; NID:g1405881; PI C;Genetics:</tax>	Query Match Query Match Best Local Similarity 35.6%; Pred: No. 1.6e-65; Matches 213; Conservative 118; Mismatches 245; Indels 22; Gaps 9;
A,Gene: Acer C,Superfamily: mammalian peptidyl-dipeptidase A	OY 4 EEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQSTLAQ 63
Query Match 31.8%; Score 1027.5; DB 2; Length 630; Beet Local Similarity 36.0%; Pred. No. 6.7e-66;	Db 22 BIQAKBYLENINKELAKRINVETEAAWAYGSNITDENEKKKNEISAELAKFWKEVASDIT 81
Matches 215; Conservative 110; Mismatches 250; Indels 23; Gaps	
OY 6 OXIT'LDKTHABADLYQSSLAAWANTNITTENVQNMNNAGLKWGYTLAKQYTLAKQYTLAKQYT 65	
	142 DLALDPEIEEVISKSRDHEELAYYWREFYDKAGTAVRSQFERYVELNTKAAKLNNFTSGA
Db ., 93 DYVQSEDADIRRQAEHLSKLGASALNADDYLALQNAISSMQTNYATATVCSYTNRSDCSL 152 OV 125 LLEPGINEIMANSLDYNERLWAWESWRSEVORCLRPLYEEYVVLKNEWARANHYEDYGDY 184	QY 183 DYWRODYBVNGVDGYDYSRQQLIBOVEHTFEBIRDLYBHHAYVRAKLMNAY-PSYISP1 241
: : :	242
Qy 185 WRGDYEVNGVDGYDYSRGQLIEDVEHTPEBIKPLYEHLHAYVRAKLMNAY-PSYISPIGC 243	MAQQWSBIADIVSPFPEKPLVDV MAQQWSBIADIVSPFPEKPLVDV SSMI,TDPGNVOKAVCHPTAWDI,GK
244 LPAHLIGDMGRFWTNLYSLTVPFGQKNIDVTDAWDQAMGRIFKEAEKFFVSGLP	312 LTKLPQDFWDKSIIBKPTDGRDLVCHASAWDFYLIDDVRIKQCTRVTQDQLFTVHHELGH
Db 263 IPISLIGNMWGQSWNELLDLFTPYPEKPFVDVKAEMEKQGYTVQKLFELGDQFFQSLGMR 322	Qy 361 1QYDWAYAAQPFLLRNGANRGFHBAVGBIWSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
Qy 304 NMTQGFWENSMLTDPGNVQKAVCHPTAWDLGK-GDFRILMCTKVTMDDFLTAHHEMGHIQ 362 123 ALPPSFWNLSVLTRPDD-RQVVCHASAWDFYQDSDVRIKMCTEVDSHYFYVVHHELGHIQ 381	Db 372 İQYFLQYQHQFFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKİĞLLK-DYVRDDEARINQ 430 Qy 421 LLKQALTIVGTLPFTYMLEKWRWNVFKGEIPKDQWMKKWWEMKRBIVGVVEPVPHDETYC 480

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Cispecies: Bacillus halodurans
Cispecies: Bacillus halodurans
Cispecies: Bacillus halodurans
Cispecies: Bacillus halodurans
Cispecies: Bacillus halodurans
Cispecies: O1-Dec-2000 #sequence_revision O1-Dec-2000 #text_change O9-Jul-2004
Ciaccession: C83696
A;Tatani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ciaccession: C83696
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83696
A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-532 <ATO>
A;Cross-references: UNIPROT:Q9KFVQ; UNIPARC:UPI00000C3863; GB:AP001508; GB:BA000004; NID: A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BH0371 [imported] - Bacillus halodurans (strain C-125)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 -----RAKLMNAYPSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGQK-PNIDVTDA
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21.1%; Pred. No. 0.002;
ive 83; Mismatches 213; Indels 144; Gaps
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| S9 DYLLGEMAASQLHHYIKT 476
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Best Local Similarity 21.1¶
Matches 118; Conservative
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DPASLFHVSNDYSFIRYYTRTLYQFQFQEALC-QAAKH-----EGPLHKCDISNSTEAGQ 534
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                                                                                                                                                                                                                                                                                             535 KLFNMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDON--KNSFVGWST 590
                                                                                                                                                                                                                                                                                                                                            RESULT 13
T15792
Hypothetical protein C42D8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15792
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19.7%; Score 635.5; DB 2; Length 9
Best Local Similarity 27.1%; Pred. No. 1.8e-37;
Matches 166; Conservative 131; Mismatches 277; Indels
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probable thermostable carboxypeptidases homolog lmol886 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004 C;Accession: AF1310 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mack, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUDD:21537279; PMID:11679669
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4.8%; Score 154; DB 2; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.003;
Matches 128; Conservative 101; Mismatches 215; Indels 192; Gaps 35;
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A,Gene: lmo1886
C,Superfamily: Zn-dependent carboxypeptidase, Taq type
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2166443 Total number of hits satisfying chosen parameters:

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SUMMARIES

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ALIGNMENTS

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TISSUE-Heart;
MEDLINE=20429895; PubMed=10969042;
MEDLINE=20429895; PubMed=10969042;
Donogline M., Haish F., Baronas E., Godbout K., Gosselin M.,
Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R.,
Breitbart R.E., Acton S.;
"A novel angiotensin-converting enzyme-related carboxypeptidase (ACE2)
converts angiotensin I.o angiotensin 1-9.";
                                                                                                                                                                                                                                        Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                 ACE2 HUMAN STANDARD; PRT; 805 AA.
09BYFI; Q6UWPO; Q86WTO; Q9NRA7; Q9UFZ6;
13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 49, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related carboxypeptidaes) (Angiotensin-converting enzyme homolog) (ACEH).
                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), TISSUE SPECIFICITY, FUNCTION, AND ENZYME REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A human homolog of angiotensin-converting enzyme. Cloning and functional expression as a captopril-insensitive carboxypeptidase."; J. Biol. Chem. 275:33238-33243 (2000).
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PubMed=15937940; DOI=10.1002/ajmg.a.30779;
Itoyama S., Keicho N., Hijikata M., Quy T., Phi N.C., Long H.T.,
Ha L.D., Ban V.V., Matsushita I., Yanai H., Kirikae F., Kirikae T.,
Kuratsuji T., Sasazuki T.;
"Identification of an alternative 5'-untranslated exon and new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [WRNA] (ISOFORM 1), TISSUE SPECIFICITY, SUBCELLULAR LOCATION, AND ENZYME REGULATION.
SUBCELLULAR LOCATION, AND ENZYME REGULATION.
PLISSUB=Testis;
Pubmed=15531706; DOI=10.1210/en.2004-0443;
Douglas G.C., O'Bryan M.K., Hedger M.P., Lee D.K.L., Yarski M.A., Smith A.I., Lew R.A.;
Smith A.I., Lew R.A.;
Fine novel angiotensin-converting enzyme (ACE) homolog, ACE2, is selectively expressed by adult Leydig cells of the testis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND VARIANT SER-638.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Circ. Res. 87:E1-E9(2000)
                                                                                                                                                                                                                      Homo sapiens (Human).
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RESULT 1
ACE2 HUMAN
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MEDINESERAIN, and Teetis;

MEDINESERAIN, and Teetis;

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MEDINESERAIN, and Teetis;

MILLINESERAIN, and T., 
                                                                                                                                                                                                                                                                                              MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).

MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;

Qlark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Clow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

Lewis L., Lison D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J.,

Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

Wood W.I., Godowski P.J., Gray A.M.,

"The secreted protein discovery initiative (SPDI), a large-scale

effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                        Suzuki Y., Watanabe M., Sugano S.; "Cloning, expression analysis and chromosomal localization of a novel "Cloning, expression analysis and chromosomal localization of a novel ACB like enzyme."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SeattleSNPB. NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The German cDNA consortium;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [8]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
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                                                                                             [5] NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
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PROTEIN SEQUENCE OF 679-689, IDENTIFICATION BY MASS SPECTROMETRY, AND INTERACTION WITH ITGEL.

PubMed=15276642; DOI=10.1016/j.bbadis.2004.05.005; Lin Q., Keller R.S., Weaver B., Zisman L.S.; "Interaction of ACE2 and integrin betal in failing human heart."; Biochim. Biophys. Acta 1689:175-178(2004).

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Li W., Greenough T.C., Moore M.U., Vasilieva N., Somasundaran M.,
Sullivan J.L., Farzan M., Choe H.,
Efficient replication of severe acute respiratory syndrome
"Efficient replication of severe acute respiratory syndrome coronavirus in mouse cells is limited by murine angiotensin-converting
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                                                                                                                                                                                                                                                                                              IDENTIFICATION BY MASS SPECTROMETRY.
PubMed=14647384; DOI=10.1038/nacure02145;
Li W., Moore M.J., Vasilieva N., Sui J., Wong S.-K., Berne M.A.,
Somasundaran M., Sullivan J.L., Luzuriaga K., Greenough T.C., Choe H.,
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ectodomain shedding of the SARS-CoV receptor, angiotensin-converting
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Vickers C., Hales P., Kaushik V., Dick L., Gavin J., Tang J.,
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PubMed=15791205; DOI=10.1038/sj.emboj.7600640;
Li W., Zhang C., Sul J., Kuhn J.H., Moore M.J., Luo S., Wong S.-K.,
Huang I.-C., Xu K., Vasiliava N., Murakami A., He Y., Marasco W.A.,
Guan Y., Choe H., Farzan M.;
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"Receptor and viral determinants of SARS-coronavirus adaptation to
                                                                                                                                                                                                                                                                             FUNCTION, INTERACTION WITH HCOV-SARS S PROTEIN, GLYCOSYLATION, AND
                                                                                       BIOPHYSICOCHEMICAL PROPERTIES, ENZYME REGULATION, AND COFACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamming I., Timens W., Bulthuis M.L.C., Lely A.T., Navis G.J., van Goor H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=15141377; DOI=10.1002/path.1570;
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Carboxypeptidase which converts angiotensin 1 to
angiotensin 1-9, a peptide of unknown function, and angiotensin II
to angiotensin 1-7, a vascadilator. Also able to hydrolyze apelin-
13 and dynorphin-13 with high efficiency. May be an important
regulator of heart function (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus (Orangutan).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                        STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQST
                                                                                                                                                                      LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
                                                                                                                                                                                                                                                                                                 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
                                                                                                                                                                                                                                                                                                                   YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP
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                                                                                                          STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                            Gaps
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13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (BC 3.4.17.-) (ACE-related
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                                             805;
PubMed=15897467; DOI=10.1073/pnas.0409465102;
Hofmann H., Pyrc K., van der Hoek L., Geier M., Berkhout
                                             Length
                                                                            0; Indels
                                          Score 3231; DB 1;
Pred. No. 4.3e-220;
0; Mismatches 0;
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13-SEP-2005 (Rel. 48, Last seq
13-SEP-2005 (Rel. 48, Last ann
                                             100.0%;
                                       Query Match
Best Local Similarity 100.
Matches 595; Conservative
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Name=ACE2;
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NCBI_TaxID=9600;
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TISSUE=Kidney
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AC QSRFN1;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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COFACTOR: Binds 1 zinc ion per subunit (By similarity).
COFACTOR: Binds 1 chloride ion per subunit (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Processing by
ADAN17 may lead to a secreted protein (By similarity).
SIMILARITY: Belongs to the peptidase M2 family.
                                                                                                                                                                                                                                                                                               EMBL, CR857122; CAH89426.1; -; mRNA.

SMR; QSRFN1; 19-615.

InterPro; IPR060622; Pept M Zn BS.

InterPro; IPR0606184; Peptidase M2.

Printry; PR01401; Peptidase M2; 1.

PRONTS; PR00791; Peptidase M2; 1.

PROSTIE; PS00142; ZINC PROTEASE; 1.

PROSTIE; PS0142; ZINC PROTEASE; 0.

Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Protease; Signal; Transmembrane; Zinc.

SIGNAL
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Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Substrate (By similarity).
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Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Chloride (By similarity).
Chloride (By similarity).
Substrate (By similarity).
N-linked (GlCNAC...) (Pot.
By similarity.
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Pred. No. 2.1e-217
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3; Mismatches
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Local Similarity 98.8%;
les 588; Conservative
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Carboxypeptidase which converts angiotensin I to
angiotensin 1-9, a peptidase which converts angiotensin II to
angiotensin 1-7, a vasodilator. Also able to hydrolyze apelin-
13 and dynorphin-13 with high efficiency. May be an important
regulator of heart function (By similarity).
-!- COFACTOR: Binds I zinc ion per subunit (By similarity).
-!- COFACTOR: Binds I chloride ion per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Processing by
ADAM17 may lead to a secreted protein (By similarity).
-!- SIMILARITY: Belongs to the peptidase M2 family.
I QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                                                                                                            379 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Laurasiatheria, Carnivora, Fissipedia, Felidae;
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Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
Metalloprotease; Protease; Signal; Transmembrane; Zinc.
SIGNAL
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13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001548; Peptidase M2.
Pfam; PF01401; Peptidase M2; 1.
PRINTS; PR00791; PEPDIPTĀSEA.
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NCBI_TaxID=9685;
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Viverridae;
Paradoxurinae; Paguma.
                                                                            13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY881174; AAX63775.1; -; mRNA.
InterPro; IPR010980; Cyt_c_b562.
InterPro; IPR066025; Pept_M_Zn_BS.
InterPro; IPR001548; Pept_dase_M2.
Pfam; PF01401; Pept_dase_M2.
PRINTS; PR00791; PEPDIPTASEA.
PROSTIE; PS00142; ZINC PROTEASE, 1
Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Protease; Signal; Transmembrane; Zinc.
SIGNAL
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Interaction with SARS S protein (By similarity).
Interaction with SARS S protein.
Interaction with SARS S protein.
Interaction with SARS S protein (By similarity).
By similarity.
                                                                                                                                                                                                                                           [1] — WOLLEOTIDE SEQUENCE, AND INTERACTION WITH HCOV-SARS S PROTEIN. Pubmed=15791205; DOJ=10.1038/8j.emboj.7600640; Li W., Zhang C., Sui J., Kuhn J.H., Moore M.J., Luo S., Wong S.-K., Hanng I.-C., Xu K., Vasilleva N., Murakami A., He Y., Marasco W.A., Guan Y., Choe H., Farzan M.; "Receptor and viral determinants of SARS-coronavirus adaptation to
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Cytoplasmic (Potential).
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                                                                                                                               carboxypeptidase).
Name=ACE2;
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402
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EMBO J. 24:16
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13-SEP-2005
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Bukaryota, Metezaoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria, Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea, Muridae; Murinae; Rattus.
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13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (BC 3.4.17.-) (ACE-related
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                            Substrate (By similarity).

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similarity)
similarity)
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85.4%; Pred. No. 4.1e-189;
ive 36; Mismatches 51;
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the Swiss Institute of Bioinformatics and the EMBL outstation
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13 and dynorphin-13 with high efficiency. May be an important regulator of heart function.
-I-COFACTOR: Binds I zinc ion per subunit (By similarity).
-I-COFACTOR: Binds I chloride ion per subunit (By similarity).
-I-ENZYME REGULATION: Activated by chloride and fluoride, but not bromide. Inhibited by MIN-4760, CFP Leu, and BDTA, but not by the bromide. Inhibited by MIN-4760, CFP Leu, and BDTA, but not by the ACE inhibitors linosipril, captopril, enalaprilat.
-I-SUBCELLULAR LOCATION: Type I membrane protein. Processing by ADAM17 may lead to a secreted protein (By similarity).
-I-TISSUE SPECIFICITY: Expressed in heart, kidney and forebrain. In testis, expressed in endothelial cells from small and large arteries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                           coronavirus in mouse cells is limited by murine angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myocardial infarction increases ACE2 expression in rat and humans.";
Eur. Heart J. 26:369-375(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arterial smooth muscle cells, and myocytes (at protein level).
Ubiquitously expressed, with highest levels in ileum, bladder and
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MISCELLANEOUS: In contrast to its human and palm-civet orthologs, does not interact with HCOV-SARS S protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=15949646; DOI=10.1016/j.peptides.2005.01.009; Gembardt F., Sterner-Kock A., Imboden H., Spalteholz M., Reibitz F., Schultheiss H.-P., Siems W.-E., Walther T.; "Organ-specific distribution of ACE2 mRNA and correlating peptidase
                                                                                                                                                                                                                                                                                                                                    Yagil Y., Penninger J.M.;
"Angiotensin-converting enzyme 2 is an essential regulator of heart function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDUCTION: Down-regulated in hypertensive animals. Up-regulated
                                      CLEOTIDE SEQUENCE [MRNA], AND LACK OF INTERACTION WITH HCOV-SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Douglas G.C., O'Bryan M.K., Hedger M.P., Lee D.K.L., Yarski M.A., Smith A.I., Lew R.A.; "The novel angiotensin-converting enzyme (ACE) homolog, ACE2, is selectively expressed by adult Leydig cells of the testis."; Endocrinology 145:4703-4711(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15671045; DOI=10.1093/eurheartj/ehi114;
Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.
                                                                        STRAIN-Sprague-Dawley;
Pubbled-15452266; DOI=10.1128/JVI.78.20.11429-11433.2004;
Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran Sulliuvan J.L., Farzan M., Choe H.;
"Efficient replication of severe acute respiratory syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the peptidase M2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=15231706; DOI=10.1210/en.2004-0443;
                                                                                                                                                                                                                                                                       PubMed=12075344; DOI=10.1038/nature00786;
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Peptides 26:1270-1277(2005)
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                                                                                                                                                                                                                                                       AND INDUCTION.
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NCBI_TaxID=10116;
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Johnston C.I.,
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the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                     R EMBL; AY881244; AAW78017.1; -; mRNA.
R RGD; 728890; Acc2.
R InterPro; IPRO06025; Pept M Zn BS.
R InterPro; IPRO01548; Peptidase_M2.
R InterPro; IPRO01548; Peptidase_M2.
R FRINTS; PRO0791; Peptidase M2; 1.
R PRINTS; PRO0791; Peptidase M2; 1.
R PROSITE; PS00678; WD REPEATS_1; 1.
R ROSITE; PS00678; WD REPEATS_1; 1.
R PROSITE; PS00142; ZINC PROTERSE; 1.
R Carboxypeptidase; Chloride; Glalo; Hydrolase; Metal-binding; M Mctalloprotease; Protease; Signal; Transmembrane; Zinc.
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(By similarity).
(By similarity).
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Extracellular (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        By similarity.
By similarity.
By similarity.
Zinc (catalytic) (By simila
Zinc (catalytic) (By simila
Zinc (catalytic) (By simila
Zinc (catalytic) (By simila
Zinc (stalytic) (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Chloride (By similarity).
Chloride (By similarity).
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N-linked (GlCNAc. . .) (F
N-linked (GlCNAc. . .) (F
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By similarity...
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NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

STRAIN=FVB/N; TISSUE=Kidney;

X MIDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Permer A.A., Rubin G.M., Hong L.,

B Aconstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Maxyo D.M., Sodergran B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Maxyo D.M., Sodergran B.J., Lu X., Gibbs R.A.,

Richards S., Worley R.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B Schnerztion and initial analysis of more than 15,000 full-length human
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LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWMKKWWBMKREIVGVVBPVPHDETYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORROTO, 099N70; 099N71; 099N71; 099N70; 099N70; 099N70; 099N71; 099N70; 099N70; 099N70; 099N70; 099N70; 099N70; 099N70; 099N71; 099N70;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDONKNSFVGWSTDWSPY
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PubMed=12075344; DOI=10.1038/nature00786; Crackower M.A., Sarao R., Oudit G.Y., Yagil C., Kozieradzki I.,

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This Swiss-Prot entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH HCOV-SARS S PROTEIN.
PubMed=15452268; DOI=10.1128/JVI.78.20.11429-11433.2004;
Li W., Greenough T.C., Moore M.J., Vasilieva N., Somasundaran M.,
Sullivan J.L., Farzan M., Choe H.;
"Efficient replication of severe acute respiratory syndrome coronavirus in mouse cells is limited by murine angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=Q8R0I0-2; Sequence=VSP 014903; Isold=Q8R0I0-2; Sequence=VSP 014903; ItSSUE SPECIFICITY: Expressed in heart, kidney and forebrain level). Ubiquitously expressed, with highest levels in leum, kidney and lung. In lung, expressed on vascular endothelial
                                                                                                                                MEDLINE=22848473; PubMed=12967627; DOI=10.1016/S0022-2828(03)00177-9; Donoghue M., Wakimoto H., Maguire C.T., Acton S., Hales P., Stagliano N., Fairchild-Huntress V., Xu J., Lorenz J.N., Kadambi V., Berul C.I., Breitbart R.E.; Heart Dlock, ventricular tachycardia, and sudden death in ACE2 transgenic mice with downregulated connexins."; J. Mol. Cell. Cardiol. 35:1043-1053(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sarao R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and airway epithelial cells.

INDUCTION: Down-regulated in lung after acute injury.

MISCELLANEOUS: Mice lacking ACES are viable and fertile, exhibit normal kidney and lung function, but show a severe reduction in cardiac contractility, and are highly sensitive to severe acute lung failure. Transgenic mice overexpressing ACES in the heart appear healthy but show conduction disturbances and ventricular arrhythmias which can lasd to sudden death.

CAUTION: Ref. il (BAB40431) sequence differs from that shown due to a frameshift in position 784.
Scanga S.E., Oliveira-dos-Santos A.J., da Costa J., Zhang L., Pei Y., Scholey J., Ferrario C.M., Manoukian A.S., Chappell M.C., Backx P.H., Yaqil Y., Penninger J.M.; "Angiotensin-converting enzyme 2 is an essential regulator of heart
                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY, INDUCTION, AND FUNCTION.

PubMed=16001071; DOI=10.1038/nature03712;

Imai Y., Kuba K., Rao S., Huan Y., Guo F., Guan B., Yang P., Sara Wada T., Leong-Poi H., Crackower M.A., Fukamizu A., Hui C.-C.,

Hein L., Uhlig S., Slutesky A.S., Jiang C., Penninger J.M.;

"Anglotensin-converting enzyme 2 protects from severe acute lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ፩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                           Virol. 78:11429-11433(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 436:112-116(2005).
                                                                                  Nature 417:822-828(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                              YGDYWRGDYEAEGADGYNYNRNQLIEDVERTFAEIKPLYEHLHAYVRRKLMDTYPSYISP
                                                                                                                                                                                 DPASLPHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGGKLFNML
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13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme 2 precursor (EC 3.4.17.-) (ACE-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
Harhay G.P., Sonstegard T.S., Clawson M.L., Heaton M.P., Keele J.W.,
Salling W.M., Weidmann R.T., Saith T.P.L.;
"Sequencing and analysis of Bos taurus full-length insert cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613
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Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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InterPro; IPR006025; Pept_M_Zn_BS.
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Name=ACE2;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                           R GO; GO: 0005615; C:extracellular space; TAS.
R GO; GO: 0005615; C:extracellular space; TAS.
R GO; GO: 0016021; C:integral to membrane; TAS.
R GO; GO: 0016021; C:integral to membrane; TAS.
R GO; GO: 00180; F: carboxypeptidase activity; TAS.
R InterPro; IPR001548; Peptidase M2.
R InterPro; IPR001648; Peptidase M2.
R InterPro; IPR001649; WD40.
R PRINTS; PR00791; PEPDIPTAEA.
R PROSITE; PS00741; PEPDIPTAEA.
R PROSITE; PS00142; ZINC_PROTEASE; 1.
R PROSITE; PS00142; ZINC_PROTEASE; 1.
W Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein; W Hydrolase; Metal-binding; Metalloprotease; Protease; Signal;
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(Potential).
(Potential).
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By similarity.
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Zinc (catalytic) (By similarity).
Zinc (catalytic) (By similarity).
Chloride (By similarity).
Substrate (By similarity).
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Extracellular (Potential).
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352 G -> E (in Ref. 1; BAB40432)
779 N -> S (in Ref. 1; BAB40431)
92368 MW, DBBB83AAC966A8D9 CRC64;
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Chloride (By similarity).
Chloride (By similarity).
Substrate (By similarity).
N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...) (Pott N-linked (GlCNAC...)) (Pott N-
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By similarity.
By similarity.
Missing (in isof
                                                                                                            EMBL; AB053181; BAB40431.1; ALT FRAME; MRNA.
EMBL; AB053182; BAB40432.1; -; MRNA.
EMBL; BC026801; AAH26801.1; -; MRNA.
                                                                                                                                                                                                                                                        Ensembl; ENSMUSG0000015405; Mus musculus.
MGI; MGI:1917258; Ace2.
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371
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515
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SMR; Q8R010; 19-615.
MEROPS; M02.006; -.
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352
379
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805 AA;
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CONFLICT
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Matches
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Best Local Similarity 61.4%;
Matches 366; Conservative 8
                                                                                    OSU380 BRARE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.
                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                  Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Whole;
                     541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 SLPYMTQGFWDNSMLTEPGDGRKVVCHPTAWDLGKGDFRIKMCTKVTMDDFLTAHHEMGH
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                            PROSITE; PS00142; ZINC PROTEASB; 1.
Carboxypeptidase; Chloride; Glycoprotein; Hydrolase; Metal-binding;
Metalloprotease; Protease; Signal; Transmembrane; Zinc.
                                                                                                                                                                                                                                                                         (Potential).
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                                                                                                                                      similarity)
similarity)
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                                                                    Angiotensin-converting enzyme
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                Substrate (By similarity). Substrate (By similarity). Substrate (By similarity). Substrate (By similarity).
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Chloride (By similarity).
Chloride (By similarity).
Substrate (By similarity).
N-linked (GlONAC. . .) (Pot
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Zinc (catalytic) (By sim
Zinc (catalytic) (By sim
Chloride (By similarity)
                                                                                               Cytoplasmic (Potential).
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(GlcNAc.
(GlcNAc.
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By similarity.
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N-linked
                                                          Potential
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InterPro; IPR001548; Peptidase M2
Pfam; PF01401; Peptidase M2; 1.
PRINTS; PR00791; PEPDIPTĀSEA.
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545
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CARBOHYD
CARBOHYD
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                                                                   CHAIN
TOPO DOM
TRANSMEM
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ACT SITE
ACT SITE
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Klausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Heishe F.,

Branchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toonlyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rabask S.A., McKernan R.J., Malke J.A., Gunzarne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Raha Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
498 DPACLFHVAEDYSFIRYYTRTIYQFQFHEALCKTAKHEGALFKCDISNSTEAGQRLLQML 557
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                  RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPY
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Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
E REAL, BCOSS667, AAHS5667.1, -; mRNA.
R ZFIN; ZDB-GENE-041114-6; zGc:92514.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR006025; Pept M Zn BS.
R InterPro; IPR001548; Peptidase M2.
R Ffam; PF01401; Peptidase M2.
R Ffam; PF01401; Peptidase M2.
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82; Mismatches 144; Indels
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PIODOM; PD004184; PEPLIGASE M3; 1.
PROSITE; PS014184; ZINC PPOTEĀSE; UNKNOWN 1.
SEQUENCE 785 ĀĀ, 90862 MW; 71CDF9488772BDB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          OSU380;
1-FRB-2005 (TrEMBLrel. 29, Created)
01-FRB-2005 (TrEMBLrel. 29, Last sequence update)
01-FRB-2005 (TrEMBLrel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=zgc:92514;
Brachydanio rerio (Zebrafish) (Danio rerio)
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NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                 299; Conservative
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preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                   319 MPAMFDNFWNNSMFIXP-EERDVVCHPTAWDMGNRKDFRIKMCTKVNMDDFLIVHHEMGH
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                                                                                                139 DCQTLEPGLESIMAESRDYDERLHVWEGWRVATGMKMRPLYEKYVDLKNEAAKLNNYEDH
                                                                                                                                                 GDYWRGDYBVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHIHAYVRAKIMNAYPSYISPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 RLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGWSTDWSP 594
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopteryygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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Genoscope; Whitehead Institute Centre for Genome Research;
Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 5 SCAF14581, whole genome shotgun sequence.
ORFNames=GSTENG00018041001;
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Nature 431:946-957(2004).
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Q4SHRO;
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NUCLEOTIDE SEQUENCE
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NamesAce; Synonyms=Dcpl;

Mesocricetus auratus (Golden hamster).

Bukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchottoglires; Girse; Rodentia; Sciurognathi; Muroidea; Cricetidae; Cricetinae; Mesocricetus.
                                                                                                                                                                                                                                                                                                                                               194 VD-GYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISPIGCLPAHLLGDM
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.

-up function converts angiotensin I to angiotensin II by release of the terminal His-Leu, this results in an increase of the vasoconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator (By similarity).

-up caralyric Activity: Release of a C-terminal dipeptide, oligopeptide-| *Asa-Ysa, when Xsa is not Pro, and Ysa is neither Asp nor Glu. Thus, conversion of angiotensin I to angiotensin II, with increase in vasoconstrictor activity, but no action on
                                                                                                                                                            Gaps
                                                                                              Length 652;
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ICE 652 AA; 75369 MW; 75784B3D18283309 CRC64;
                                                                                           49.9%; Score 1613; DB 2;
64.2%; Pred. No. 1.6e-105;
ive 58; Mismatches 105;
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13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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GDSWRSSYBSKSLE------QDLEQLYQELQPLYLNLHAYVRRSLHRHYGSQHINL
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AC P22966;
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                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin-converting enzyme, somatic
                                                                                                                                                                                                                                                                                                                   Pfam; PF01401; Peptidase M2; 2.
PROSITE; PS00142; ZINC PROTEASE; 2.
Alternative splicing; Čarboxypeptidase; Glycoprotein; Hydrolase;
Metal-binding; Metalloprotease; Phosphorylation; Protease; Repeat;
                                                                                  Isoid=Q50JE5-1; Sequence=Displayed;
Name=Testla - specific;
Isoid=Q50JE5-2; Sequence=Not described;
FTM: Phosphorylated by CK2 on Ser-1307; which allows membrane
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similarity).
similarity).
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COPACTOR: Binds 2 chloride ions per subunit (By similarity) SUBCELLUIAR LOCATION: Type I membrane protein. A soluble for released by proteolysis also exists (By similarity). ALTENNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
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3 include 2 (By similarity).
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7 include 6 (GlOMAC. .) (Potentialy).
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Peptidase M2 1.
Peptidase M2 2.
                                                                                                                                             retention (By similarity).
-!- SIMILARITY: Belongs to the peptidase M2 family.
                                                          Event=Alternative splicing; Named isoforms=2,
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InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001548; Peptidase M2.
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
241 IGCLPAHLLGDMWGRFWTNLYSLTVPFGQKPNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
                       CDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNM
                                                                                     GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DPRILMCTKVTMDDFLTAHHEMG
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MEDLINE=89338720; PubMed=2547653; DOI=10.1016/0014-5793(89)80897-X;
Lattion A.L., Soubrier F., Allegrini J., Hubert C., Corvol P.,
Alhenc-Gelas F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99251580; PubMed=10319862; DOI=10.1038/8760;
Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
Sequence variation in the human angiotensin converting enzyme.";
Nat. Genet. 22:59-62(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
13-SEP-2005 (Rel. 19, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, testis-specific isoform precursor (EC 3.4.15.1) (EC 3.2.1.-) (ACE-T) (Dipeptidyl carboxypeptidase I (Kininase II) [Contains: Angiotensin-converting enzyme, testis-specific isoform, soluble form].
Name=ACE; Synonyms=DCP, DCP1;
Homo sapiens (Human).
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MEDLINE=90046671; Pubmed=2554286;
Ehlers M.R.W., Fox E.A., Strydom D.J., Riordan J.F.;
"Molecular cloning of human testicular anglotensin-co
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GO; GO:0004246; F:peptidyl-dipeptidase A activity; TAS.

GO; GO:000508; P:proteolysis and peptidolysis; TAS.

GO; GO:000508; P:proteolysis and peptidolysis; TAS.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR001548; Peptidase M2.

PERMITS; PR00191; Peptidase M2; 1.

PRINTS; PR00191; Peptidase M2; 1.

PROSTIE; PS00142; ZINC PROTEASE; 1.

PROSTIE; PS00142; ZINC PROTEASE; 1.

PROSTIE; PS00142; Alternative splicing; Carboxypeptidase; Chloride; Glycoprotein; Glycosidase; Hydrolase; Metal-binding; Metalloprotease; Phosphorylation, Polymorphism; Protease; Signal; Testis;
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PDB; 10086; X-ray; A=66-556.

PDB; 1008A; X-ray; A=66-656.

PDB; 10ZE; X-ray; A=68-656.

PDB; 10ZE; X-ray; A=68-656.

RISEMD!, RNSG0000015940; Homo sapiens.

HGNC; HGNC: 2707; ACE.
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  IsoId=P22966-1; Sequence=Displayed;
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EMBL; X16295; CAA34362.1; -; mRNA.
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  PARAPERISTALLOGRAPHY (1.8 ANGSTROMS) OF 68-656 IN COMPLEX WITH ENALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH CAPTOPRIL.

COMPLEX WITH CAPTOPRIL.

RUDMEd-15236580; DOI-10.1021/bi049480n;

Natesh R., Schwager S.L.U., Evans H.R., Sturrock E.D., Acharya K.R.;

"Structural details on the binding of antihypericansive drugs captopril

and enalaprilat to human testicular angiotensin I-converting enzyme.";

Biochemistry 43:8718-8724(2004).

I FUNCTION: Converts angiotensin I to angiotensin II by release of the the terminal His-Leu, this results in an increase of the vasoconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator. Has also a glycosidase activity which releases GPI-anchored proteins from the membrane by cleaving the mannose linkage in the GPI modety.

C.I. GATALYTIC ACTIVITY: Release of a C-terminal dipeptide,

C.I. GATALYTY (ACTIVITY: Release of a C-terminal dipeptide).

C.I. CATALYTON TOWNSTION of angiotensin I to angiotensin II, with increase in vasoconstrictor activity, but no action on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=12459472;
Harmer D., Gilbert M., Borman R., Clark K.L.;
"Quantitative mRNA expression profiling of ACE 2, a novel homologue of anglotensin converting enzyme.";
                                                      MEDLINE=96302256; PubMed=8755737; DOI=10.1021/bi960243x; MEDLINE=96302256; PubMed=8755737; DOI=10.1021/bi960243x; Sturrock E.D., Yu. X.C., Wu Z., Biemann K., Riordan J.F.; "Assignment of free and disulfide-bonded cysteine residues in testis angiotensin-converting enzyme: functional implications."; Biochemistry 35:9560-9566(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656, AND X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 68-656 IN COMPLEX WITH LISINOPRIL. PubMed=12540854; DOI=10.1038/nature01370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KW=2.7 mM for Hip-His-Leu;
SUBCELLULAR LOCATION: Type I membrane protein. A soluble form
released by proteolysis also exists.
ALTERNATIVE PRODUCTS:
Event=Alternative alplicing; Named isoforms=2;
Name=Testis-specific;
                                                                                                                                                                                                                CARBOHYDRATE-LINKAGE SITES ASN-121; ASN-140; ASN-186; ASN-368 AND ASN-617, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12542396; DOI=10.1042/BJ20021842;
Gordon K., Redelinghuys P., Schwager S.L.U., Ehlers M.R.W.,
Papageorgiou A.C., Natesh R., Acharya K.R., Sturrock B.D.;
"Deglycosylation, processing and crystallization of human testis
angiotensin-converting enzyme.";
Blochem. J. 371:437-442(2003).
                                                                                                                                                                                                                                                                                             Yu X.C., Sturrock B.D., Wu Z., Biemann K., Ehlers M.R.W., Riordan J.F., "Identification of N-linked glycosylation sites in human testis angiotensin-converting enzyme and expression of an active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natesh R., Schwager S.L.U., Sturrock E.D., Acharya K.R.;
"Crystal structure of the human angiotensin-converting enzyme-
lisinopril complex.";
Nature 421:551-554(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOPHYSICOCHEMICAL PROPERTIES, AND CLEAVAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 272:3511-3519(1997).
Biochemistry 30:7118-7126(1991)
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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                                                                                                                                                                                                                                                                                                  Length 732;
                                             /FTId=vAR 011710.

S - S (in dbSNP:4318).

/FTId=vAR 011711.

/FTId=vAR 023435.

I -> T (in dbSNP:4976).
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                            (in dbSNP:4317)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Angiotensin I converting enzyme, isoform 3.
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Coherration and initial analysis of more than 15,000 full-length human
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al Similarity 41.9%; Pred. No. 9.5e-86;
254; Conservative 116; Mismatches 202; Indels 34; Gaps
                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Director MGC Project;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036375; AAH36375.1; -; mRNA.
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Ensembl; ENSG0000155640; Homo sapiens.
GO; GO:0016202 c:membrane; IEA.
GO; GO:0006246; P:peptidyl-dipeptidase A activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001248; Peptidase M2.
InterPro; IPR001248; Pept M Zn_BS.
Pfam; PF01401; Peptidase_M2; 1.
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ProDom; PD004184; Peptidase M2; 1.
PROSITE; PS00142; ZINC PROTEÄSE; UNKUOWN 1.
SEQUENCE 713 AA; 83§58 MW; 87995DFF58D93D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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NUCLEOTIDE SEQUENCE.
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SMR; Q8N710; 71-64
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                                                                                                                                                                                                                                                                 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
                                                                             412 EDNETEINFLLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P12821; Q53YX9; Q59GY8;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, somatic isoform precursor (EC 3.4.15.1)
(Dipeptidyl carboxypeptidase I) (Kininase II) (CD143 antigen)
[Contains: Angiotensin-converting enzyme, somatic isoform, soluble
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                     SD-EHDINFLMKMALDKIAPIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCP
                                                                                                                                                                                     PVPHDETYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89071703; PubMed=2849100; Soubrier F., Alhenc-Gelas F., Hubert C., Allegrini J., John M., Tregear G., Corbol P.; Twegear G., Corbol P.; Two putative active centers in human angiotensin I-converting enzyme revealed by molecular cloning."; Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS SER-261; TRP-561 AND
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Rieder M.J., Taylor S.L., Clark A.G., Nickerson D.A.;
"Sequence variation in the human angiotensin converting enzyme.";
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Ohara O., Nagage T., Kikuno F.R.;
Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification of human lung angiotensin-converting enzyme by performance liquid chromatography: properties and N-terminal acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 1-1239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1306 AA.
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PARTIAL PROTEIN SEQUENCE OF 30-46.
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MEDLINE=91308093; PubMed=1649623;
Ehlere M.R.W., Riordan J.F.;
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NUCLEOTIDE SEQUENCE [MRNA]
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Donoghue M., Haieh F., Baronas E., Godbout K., Gosselin M., Stagliano N., Donovan M., Woolf B., Robison K., Jeyaseelan R., Breitbart R.E., Acton S., M. a., 
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"Quantitative mRNA expression profiling of ACB 2, a novel homologue angiotensin converting enzyme.";
FBBS Lett. 532:107-110(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exries M., Michaud A., Deinum J., Agrapart M., Chomilier J., Kramers C., Soubrier F., Increased shedding of angiotensin-converting enzyme by a mutation identified in the stalk region.";
J. Biol. Chem. 276:5525-5532(2001).
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PubMed=15671045; DOI=10.1093/eurheartj/ehill14;
Burrell L.M., Risvanis J., Kubota E., Dean R.G., MacDonald P.S.,
Lu S., Tikellis C., Grant S.L., Lew R.A., Smith A.I., Cooper M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Shedding of somatic angiotensin-converting enzyme (ACE) is
inefficient compared with testis ACB despite cleavage at identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Woodman Z.L., Oppong S.Y., Cook S., Hooper N.M., Schwager S.L.U., Brandt W.P., Ehlers M.R.W., Sturrock E.D.; "Shedding of somatic angiotensin-converting enzyme (ACE) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of N-linked glycosylation sites in human testis angiotensin-converting enzyme and expression of an active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB SPECIFICITY.
MEDLINE=20517872; PubMed=10924499; DOI=10.1074/jbc.M002615200;
"Angiotensin-converting enzyme: zinc- and inhibitor-binding stoichiometries of the somatic and testis isozymes."; Biochemistry 30:7118-7126(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                            Yu X.C., Sturrock B.D., Wu Z., Biemann K., Ehlers M.R.W.,
Riordan J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A human homolog of angiotensin-converting enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11076943; DOI=10.1074/jbc.M007706200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 272:3511-3519(1997).
                                                                                                                                                                                                                                                                                                                               AND ASN-942, AND MASS SPECTROMETRY
PubMed=9013598;
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MEDLINE=20429895; PubMed=10969042;
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Biochem. J. 347:711-718(2000)
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                                                                     MEDLINE=99318094; Pubmed=10391210; Don=10.1038/10297.

A Gooper K., Lipshutz K., Chakravarti A.;
Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
Cooper K., Lipshutz K., Chakravarti A.;
"Patterns of single-nucleotide polymorphisms in candidate genes for blood-pressure homeostasis.";

I Nat. Genet. 22:339-247(1939).

-! FUNCTION: Converts angiotensin I to angiotensin II by release of the terminal His-Leu, this results in an increase of the vasconstrictor activity of angiotensin. Also able to inactivate bradykinin, a potent vasodilator.

-! CATALVIIC ACTIVITY: Release of a C-terminal dipeptide, oligopeptide-|-Xaa-Yaa, when Xaa is not Pro, and Yaa is neither Asp nor glu. Thus, conversion of angiotensin II, with increase in vasoconstrictor activity, but no action on angiotensin II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=P12821-1; Sequence=Displayed;
Name=Testies-specific;
Isold=P22966-1; Sequence=External;
-!- TISSUE SPECIFICITY: Ubiquitously expressed, with highest levels in lung, kidney, heart, gastrointestinal system and prostate.
-!- INDUCTION: Up-regulated in failing heart.
-!- PTM: Phosphorylated by CK2 on Ser-1299; which allows membrane
Johnston C.I.; "Myocardial infarction increases ACB2 expression in rat and humans.";
                                                                                                                                                                                                                                                                                                                 COFACTOR: Binds 2 zinc ions per subunit (By similarity).
COFACTOR: Binds 2 chloride ions per subunit (By similarity).
ENZYME REGULATION: Strongly activated by chloride. Specifically inhibited by lisinopril, captopril and enalaprilat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01401; Peptidase_M2; 2.
PRINTS; PR00791; PEPDIPTAGEA.
PRODOM; PD004184; Peptidase M2; 2.
PROSITE; PS00142; 21NC PROTEASE; 2.
Alternative splicing; Carboxypeptidase; Direct protein sequencing;
                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. A soluble form released by proteolysis also exists.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retention.
--- MSCELLANBOUS: Inhibitors of ACE are commonly used to treat hypertension and some types of renal and cardiac dysfunction.
--- SIMILARITY: Belongs to the peptidase M2 family.
                                               [15]
VARIANTS THR-1018; VAL-1051; GLN-1279; SER-1286 AND PRO-1296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:000517; P:regulation of blood pressure; TAS.
InterPro; IPR006025; Pept M. Zn. BS.
InterPro; IPR001548; Peptidase_M2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J04144; AAA51684.1; -; mRNA.
EMBL; AF118569; AAD28560.1; -; Genomic_DNA.
EMBL; AX436326; AAR03564.1; -; Genomic_DNA.
EMBL; A3436356; AR092208.1; ALT_INIT; mRNA.
PIR; A31759; A31759.
HSSP; Q10714; 1J36.
SMR; P12821; 645-1222.
MEROPS; M02.001; -.
MEROPS; M02.004; -.
ENGEMDE; ENGG00000159640; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                     inhibited by lisinopril, captor BIOPHYSICOCHEMICAL PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                   KM=2.51 mM for Hip-His-Leu;
                             Heart J. 26:369-375(2005).
                                                                                                                                                                                                                                                                                                                                                                                                    Kinetic parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC; HGNC:2707; ACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Somatic;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Angiotensin-converting enzyme, testis-specific isoform precursor (RC 3-4.15.1) (RC 3.2.1.-) (ACE-T) (Dipoptidyl carboxypeptidase 1 (Kininase II) [Contains: Angiotensin-converting enzyme, testis-specific isoform, soluble form].
                                                                                                                                                                                                                                                                                                                                                34;
                                                                                                                                                                                                                                               Length 1306;
                                                                                                                                                                                                                                                                                                                                                Indels
Glycoprotein, Hydrolase, Metal-binding, Metalloprotease, Phosphorylation, Polymorphism, Protease, Repeat, Signal,
                                                                                                                                                                                                                                          tch
al Similarity 41.9%; Pred. No. 2.1e-85;
254; Conservative 116; Mismatches 202;
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NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA]
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Mus musculus (Mouse).
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                                                                                                          Transmembrane; Zinc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- MISCELLANEOUS: Mice lacking ACE have low blood pressure, elevated gerum potassium, anemia, and renal defects. Male mice have reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=15665832; DOI=10.1038/nm1179;
Kondoh G., Tojo H., Nakatani Y., Komazawa N., Murata C., Yamagata K.,
Maeda Y., Kinoshita T., Okabe M., Taguchi R., Takeda J.;
"Angiotensin-converting enzyme is a GPI-anchored protein releasing
factor crucial for fertilization.";
                                       K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [4]
FUNCTION, ENZYME REGULATION, AND MUTAGENESIS OF HIS-413; GLU-414 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Esther C.R. Jr., Howard T.E., Marino E.M., Goddard J.M.,
Capecchi M.R., Bernstein K.E.;
"Mice lacking angiotensin-converting enzyme have low blood pressure,
renal pathology, and reduced male fertility.";
Lab. Invest. 74:953-965(1996).
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                                                                                                                                                                                                                               Krege J.H., John S.W., Langenbach L.L., Hodgin J.B., Hagaman J.R., Bachman E.S., Jennette J.C., O'Brien D.A., Smithies O.; "Male-female differences in fertility and blood pressure in ACE-
MEDLINE=90318396; PubMed=2164636; Howard T.E., Shai S.-Y., Langford K.G., Martin B.M., Bernstein K. Transcription of testicular angiotensin-converting enzyme (ACE) intitated within the 12th intron of the somatic ACE gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- INDUCTION: Expression is thought to be subject to hormonal regulation by androgens.
-1- PTM: Phosphorylated by CK2 on Ser-725; which allows membrane retention (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Spermatocytes, adult testis.
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IsoId=P22967-1; Sequence=Displayed;
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                                                                                                                                                                                                         PubMed=7753170; DOI=10.1038/375146a0;
                                                                                                                                                                                                                                                                                                                                              Nature 375:146-148(1995).
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EMBL; M55333; AAA37149.1; -; mRNA. EMBL; M61094; AAA37150.1; -; Genomic_DNA.

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                                                                                                                                                                                                                                                                                                                                                                           Angiotensin-converting enzyme, testis-
specific lasform, soluble form.
Removed in secreted form (By similarity)
Extracellular (Potential).
                                                              R KIBSHMA1; ALC.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0016021; C:integral to membrane; TAS.

R InterPro; IPR0060525; Pept M Zn BS.

R InterPro; IPR0060548; Peptidase M2; 1.

DR Pfam; PF01401; Peptidase M2; 1.

DR PRODITE; PS00142; ZINC PROTEASE.

DR PROSITE; PS00142; ZINC PROTEASE; 1.

RNSTER; PS00142; ZINC PROTEASE; 1.

RN Alternative splicing; Garboxypeptidase; Chloride; Glycoprotein; KW Alternative splicing; Garboxypeptidase; Transmembrane; Zinc.

RN Glycosidase; Hydrolase; Metal-binding; Metalloprotease;

KW Phosphorylation; Protease; Signal; Testis; Transmembrane; Zinc.

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By Ximilarity beptidase activity but effect on GPIase activity, when
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E->D: Abolishes peptidase activity but
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specific isoform.
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N-linked (GlcNAc. ..) (complex) (By
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N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
N-linked (GlCNAc. . .) (Potential).
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16C817E7FBD09BD9 CRC64;
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PIR; A35655; A35655.
HSSP; Q10714; 1J36.
SMR; P22967; 70-647.
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARAUSPER R.L., Feingold E.A., Grouse L.H., Derge J.G.,

MISCAUL S.F., Collins F.S., Magner L., Schner G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mischen R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenco L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

Norstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Bronnerch A., Schein J.E., Jones B.D., Dickson M.C.,

Bronnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Bronnerch A., Schein J.E., Jones J.M., Marra M.A.,

Bronnerch A., Schein J.E., Jones B.D., Dickson M.C.,

Bronnerch A., Schein 
                               247 GDSWRSLYESDNLE------QDLEKLYQELQPLYLNLHAYVRRSLHRHYGSEYINL 296
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                                                                                                                                                                         297 DGPIPAHLIGNMWAQTWSNIYDLVAPFPSAPNIDATEAMIKQGWTPRRIFKEADNFFTSL 356
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034367; AAH34367.1; -; mRNA.
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Last annotation update)
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STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
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Ace protein (Fragment).
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41.3%; Score 1334; DB 2; Length 1
Best Local Similarity 42.6%; Pred. No. 1.7e-85;
Matches 255; Conservative 112; Mismatches 213; Indels
                                                                                                                                                                                                                                                                      1015 AA; 117509 MW; D097F6958553C27 CRC64;
HSSP, Q10714; 1J37.

SMR; Q8K233; 416-993.

MGI; MGI: 9005615; Ace.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR001548; Peptidase_M2.

InterPro; IPR006025; Pept M Zn_BS.

Pfam; PF01401; Peptidase M2; 2.

PRINTS; PR00719; PEPDIPTĀSEA.

PROSTIE; PS00142; ZINC_PROTEASE; UNKNOWN_2.
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SEQUENCE
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earch completed: March 28, 2006, 11:16:07 ob time : 126.785 secs

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APPLICANT: PANTOLIANO, MICHAEL W.
APPLICANT: RYAM, M. DOMINIC
APPLICANT: RYAM, M. DOMINIC
APPLICANT: RYAM, M. DOMINIC
APPLICANT: RYAM, M. DOMINIC
APPLICANT: TANO, G. SRIDHAR
APPLICANT: TANO, JIN
APPLICANT: TOWLER, PAUL S.
APPLICANT: PISHER, MARTIN
TITLE OF INVENTION: CRYSTAL STRUCTURE OF ANGIOTENSIN-CONVERTING ENZYME-RELATED
TITLE OF INVENTION: CARGOXYPEPTIDASE
FILE REFERENCE: MNM/002
CURRENT APPLICATION NUMBER: 120/10/659,000
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 60/410,010
PRIOR PILING DATE: 2002-09-09
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US-10-176-921-72
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US-10-123-419-72
US-10-123-429-72
US-10-142-423-72
US-10-142-423-72
US-10-142-423-72
US-10-142-423-72
US-10-143-032-72
US-10-123-261-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%;
Matches 595; Conservative 0;
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SOFTWARE: Patentin Ver. 3.2
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US-10-188-847-142
US-10-005-956-570
US-10-005-956-843
US-10-158-825-142
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Maximum Match 100%
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                                                   GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
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; Sequence 2, Application US/0999781
; Publication No. US20040082496A1
; GENERAL INFORMATION:
; APPLICANT: ACTOM, SUSAN L.
; APPLICANT: GOLIN, TIMOTHY D.
; APPLICANT: GOLIN, TIMOTHY D.
; APPLICANT: GOLIN, BINGS A.
; APPLICANT: GOLIN, BINGS A.
; APPLICANT: BAROM, JAMES A.
; APPLICANT: BAROM, MICHAEL
; APPLICANT: STRICKER-KRONGRAD, ALAIN
; APPLICANT: STRICKER-KRONGRAD, ALAIN
; APPLICANT: STRICKER-KRONGRAD, ALAIN
; TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND METHODS
; TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS
; TITLE OF INVENTION WHERE: US/09/999, 781
; CURRENT APPLICATION NUMBER: US/09/999, 781
; PRIOR PILING DATE: 2001-05-29
; PRIOR PILING DATE: 2001-05-29
; PRIOR PILING DATE: 2001-10-11
; PRIOR PILING DATE: 2001-10-19
; PRIOR FILING DATE: 2001-10-19
; PRIOR PILING DATE: 2001-10-19
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; ORGANISM: Homo sapiens
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JOS-097978-383-5

Patent No. US20020177211A1

GENERAL INFORMATION:

APPLICANT: Piddington, Christopher S.

APPLICANT: Petrie, Charles

APPLICANT: Bishop, Paul D.

TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME

FILE REFERENCE: 99-24C1

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 05/133,952

PRIOR APPLICATION NUMBER: 60/131,952

PRIOR PILING DATE: 1999-05-13

PRIOR FILING DATE: 1999-05-13

PRIOR FILING DATE: 1999-06-27

PRIOR FILING DATE: 2000-05-03

NUMBER OF SEQ ID NOS: 11

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LENGTH: 805
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Best Local Similarity 100.
Matches 595; Conservative
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GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH
                                                                1QYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
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TITLE OF INVENTION: HUMAN SINGLE NUCLECTIDE POLYMORPHISMS
FILE REFERENCE: D0053NP
CURRENT APPLICATION NUMBER: US/10/005,956
CURRENT FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/251,015
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 60/263,678
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 60/273,037
PRIOR APPLICATION NUMBER: 2001-01-03-02
SOFTWARE: PALGATION VERSION 3.0
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US-10-005-956-570
Sequence 570, Application US/10005956
Publication No. US20030113726A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-005-956-570
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Publication No. US20030091557A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF557
CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 142
LENGTH: 805
259 IGCLPAHILGDMWGRFWTNLYSLTVPFGQXFNIDVTDAMVDQAWDAQRIFKEAEKFFVSV
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; ORGANISM: homo sapiens
US-10-158-847-142
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US-10-158-847-142
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Oy 361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420 	~ 6	421 LLKQALTIVGTLPFTYMLEKWRWNVPKGEIPKDQMMKKWWEMKRRIVGVVEPVPHDETYC 480
421 LLKOALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC 480 	ζό g	481 DPASLEHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540
481 DPASLFHVSNDYSFIRYYTRILYQFQFQBALCQAAKHEGPLHKCDISNSTEAGQKLFNML 540 	δ O	541 RLGKSEPWTLALENVVGAKNANVRPLLANYEBLFTWLKDQNKNSFVGWSTDWSPY 595
541 RLGKSEPWTLALENVVGAKNMNVRPLLNYPEPLFTWLKDQNKNSFVGWSTDWSPY 595 	RESULT OS-10-19	RESULT 7 US-10-158-825-142 ; Sequence 142, Application US/10158825
RESULT 6 US-10-005-956-843 Sequence 843, Application US/10005956 Sequence 843, Application US/10005956 Sequence 843, Application US/10005966 SERREAL INFORMATION: APPLICANT: Bristol-Myers Squibb Company TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS FILE REFERENCE: D0053NP CURRENT FILING DATE: 2001-12-03 PRIOR PELLING DATE: 2001-12-03 PRIOR APPLICATION NUMBER: 60/251,015 PRIOR FILING DATE: 2001-01-23 PRIOR APPLICATION NUMBER: 60/263,678 PRIOR PLILING DATE: 2001-01-23 PRIOR APPLICATION NUMBER: 60/273,037	Public GRUERA APPLIC TITLE TITLE CURRE PRIOD PRIOD SOFT SEQ II SEQ II TYPE TYPE US-10-11	Publication No. US2030138894A1 GENERAL INFORMATION: GENERAL INFORMATION: TYTLE OF INVENTION: Method and Compositions for Modulating ACB-2 Activity TITLE OF INVENTION: Method and Compositions for Modulating ACB-2 Activity TITLE OF INVENTION UNBER: US/10/158,825 CURRENT APPLICATION NUMBER: 60/294,976 FRIOR PELING DATE: 2001-06-04 NUMBER OF SEQ ID NOS: 158 SOFTWARE: PATENTIN VERSION 3.1 SEQ ID NO 142 LENGTH: 805 TYPE: PRT ORGANISM: homo sapiens
PRIOR FILING DATE: 2001-03-02 NUMBER OF SEQ 1D NOS: 1579 SECTWARE: Patentin version 3.0	Query M Best Loo Matches	Query Match Best Local Similarity 100.0%; Score 3231; DB 4; Length 805; Best Local Similarity 100.0%; Pred. No. 2.4e-273; Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; LEMELTH: BUS ; ORGANISM: homo mapiens US-10-005-956-843	& g	1 STIEEQAKTFLDKFNHEAEDLFYQSSLASMYNTNITEENVQNMNNAGDKWSAFLKEQST 60
Query Match Best Local Similarity 100.0%; Score 3231; DB 4; Length 805; Best Local Similarity 100.0%; Pred. No. 2.4e-273; Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	<i>₹</i> 0 €	61 LAQMYPLQEIQNLTVKLOLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120
1 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEGST 60 	δ qa	121 QECLLIEPGINEIMANSLDYNERLWAWESKRSEVGKQLRELYEEYVVIKNEMARANHYED 180
61 LAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP 120 	čo qa	181 YGDYWRGDYEVNGYDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
121 QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEWARANHYED 180 	रु व	241 IGCLPAHLIGDMWGRFWTNLYSLTVPFGGKENIDVTDAWVDQAWDAQRIFKEAEKFFVSV 300
181 YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEBIKPLYEHLHAYVRAKLANNAYPSYISP 240 	çy Qa	301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360
241 IGCLPAHLLGDWWGRFWTNLYSLTVPFGQRPNIDVTDAWVDQAWDAQRIFKEAEKFFVSV 300 	ço,	361 IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420
301 GLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHEMGH 360 	δδ qα	421 LLKQALTIVGTLPFTYMLEKWRWWVFKGEIPKDQWWKKWWBMKREIVGVVEPVPHDETYC 480
361 IQYDMAYAAQPFLIRNGANEGFHEAVGBIMSLSAATPKHLKSIGLLSPDFQEDNETEINF 420 	ζο qa	481 DPASLFHVSNDYSFIRYYTRTLYQFQFQBALCQAAKHEGFLHKCDISNSTBAGQKLFNML 540
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                                                                              Sequence 142, Application US/10158825
Publication No. US20040121429A9
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF555
CURRENT PELLING NUMBER: 08/10/158,825
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 142
                                                                                                                                                                                                                                                                                                                                                                                    19 STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQST
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Best Local Similarity 100.0%; Pred. No. 2.4e-273;
Matches 595; Conservative 0; Mismatches 0;
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; ORGANISM: homo sapiens
US-10-158-825-142
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RESULT 9 US-10-756-149-5456 ; Sequence 5456, Application US/10756149

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Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Alexana
APPLICANT: Zlotnik, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
TITLE OF INVENTION: NOTEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REPERENCE: file
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARER PATENTAL ASSESSION OF SEG ID NOS: 5818
SEQ ID NO 5456
LENGTH: 805
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TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: DIAGNOSTIC USES THEREFOR
FILE REPERENCE: MNI-13202P3
CURRENT APPLICATION NUMBER: US/11/059,218
CURRENT FILING DATE: 2005-02-16
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100.0%; Pred. No. 2.4e-273;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 595; Conservative
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5456
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PRIOR FILING DATE: 2000-08-US
PRIOR APPLICATION NUMBER: 09/407,427
PRIOR FILING DATE: 1999-09-29
PRIOR PILING DATE: 1998-09-30
PRIOR PLLING DATE: 1998-09-30
PRIOR PLLING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 106
                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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100.0%; Pred. No. 2.4e-273;
ative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US/09/635,501
PRIOR FILING DATE: 2000-08-09
PRIOR PILING LATE: 1999-09-29
PRIOR PILING DATE: 1999-09-29
PRIOR PILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATCHIN VERY OF SEQ ID NOS: 107
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Best Local Similarity 100.
Matches 595, Conservative
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US-11-059-218-2
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                                                                                                                                                                         STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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                                                                                            Gaps
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0
                                           Length 805;
                                                                                            0; Indels
                                           100.0%; Score 3231; DB 6;
100.0%; Pred. No. 2.4e-273;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 86, Application US/10114893; Publication No. US20020193567A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Colling-Racie, Liea A
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
                                                                     Best Local Similarity 100.
Matches 595; Conservative
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US-11-059-218-106
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US-10-114-893-86
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Sequence 106, Application US/11059218
Publication No. US20850147600A1
GENERAL INFORMATION:
APPLICANT: Acton, Susan L. et al.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
TITLE OF INVENTION: DAGNOSTIC USES THEREFOR
FILE REFERENCE: MNI-132CP3
CURRENT FILING NUMBER: US/11/059,218
CURRENT FILING DATE: 2005-02-16
PRIOR APPLICATION NUMBER: US/09/635,501

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Sequence 140, Application US/10158847; Publication No. US20030091557A1
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US-10-158-847-140
                                                                                                                                                   LENGTH: 681
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Publication No. US20020192749A1
GENERAL INFORMATION:
APPLICANT: Moore, et al.
TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
FILE REPRENEUE: PFOSSP1
CURRENT APPLICATION NUMBER: US/09/969,384
CURRENT FILING DATE: 2001-10-03
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APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelry S.
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REPERBENC: G1 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT PILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNML
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99.8%; Pred. No. 5.4e-273;
tive 1; Mismatches 0;
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Best Local Similarity 99.8<sup>1</sup>
Matches 594; Conservative
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-10-114-893-86
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                                                                                                                                                                                                                                                                                                                                                                               naturally occurring L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE

LOCATION: (499)

COTATION: (A99)

OTHER INFORMATION: Xaa equals any of the naturally occurring US-09-969-384-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 92.4%; Score 2987; DB 3; Length 681;
Best Local Similarity 99.3%; Pred. No. 4.3e-252;
Matches 548; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xaa equals any of the naturally occurring
                                                                                                                                                                                                                                                                                                                                                                               of the
       PCT/US01/10542
PRIOR APPLICATION NUMBER: PCT/USO1/1054
PRIOR FILING DATE: 2001-04-02
PRIOR PRICATION NUMBER: 60/236,384
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER: OF SEQ ID NOS: 27
SEQ ID NO 25
                                                                                                                                                                                                                                                   TYPE: PRT
ORCANISM: Homo sapiens
ORCANISM: Homo sapiens
FATURE:
NAME/KEY: SITE
LOCATION: (219)
OTHER INFORMATION: Xaa equals any of
NAME/KEY: SITE
LOCATION: (240)
OTHER INFORMATION: Xaa equals any of
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241 WDAQRIFKGAEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKGDFRILMC 300
                                                                           APPLICANT: TOM PAIRY et al.

TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PP555
CURRENT APPLICATION NUMBER: US/10/158,825
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/294,976
PRIOR PILING DATE: 2001-66-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 140
LENGTH: 681
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99.3%; Pred. No. 4.3e-252;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (219). (219)
OTHER INFORMATION: Xaa equals any amino acid FEATURE:
NAME: NAME: FEATURE
LOCATION: (240). (240)
OTHER INFORMATION: Xaa equals any amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (499)
THER INFORMATION: Xaa equals any amino acid
US-10-158-825-140
                 Sequence 140, Application US/10158825
Publication No. US20030138894A1
GENERAL INFORMATION:
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Matches 548; Conservative
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ORGANISM: homo sapiens
FEATURE:
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  US-10-158-825-140
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APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF557
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Pred. No. 4.3e-252;
0; Mismatches 4;
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: homo sapiens
FBATURE:
NAME/KEY: MISC FEATURE
LOCATION: (219)..(219)
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240).
OTHER INFORMATION: Xaa equals any amino acid
FEATURE:
FEATURE:
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1. OTHER INFORMATION: Xaa equals any amino acid
US-10-158-847-140
                                                        CURRENT APPLICATION NUMBER: US/10/158,847
CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: Patentin version 3.1
SEQ ID NO 140
LENGTH: 681
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Best Local Similarity 99.3:
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139 QECLLIEPGINEIMANSIDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
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100.0%; Pred. No. 1.3e-252;
tive 0; Mismatches 0;
                                        US-110-878-556A-25
US-10-793-626-1212
US-10-515-547-6
US-10-515-547-6
US-10-310-773-499
US-11-0329-6748
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US-11-029-465-10
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ORGANISM: Homo sapiens US-10-518-599-2
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Sequence 1021, Appl
Sequence 502, Appl
Sequence 506, Appl
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APPLICANT: Farran, Michael R
APPLICANT: Farran, Michael R
APPLICANT: Brigham & Women's Hospital, Inc.
APPLICANT: Brigham & Wonel R
APPLICANT: More, Michael J
TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Coronav
TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Coronav
CURRENT APPLICATION NUMBER: US/10/957,880
CURRENT FILING DATE: 2004-10-05
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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Best Local Similarity 100.0%; Pred. No. 1.2e-251;
Matches 592; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-957-880-2
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APPLICANT: L1, Wenhul
APPLICANT: L1, Wenhul
APPLICANT: L1, Wenhul
APPLICANT: Moore, Michael J
TITLE OF INVENTION: Angiotensin-Converting Enzyme-2 as a Receptor for the SARS Corona
FILE REPERENCE: 7570/80644
CURRENT APPLICATION NUMBER: US/10/957,880
CURRENT FILING DATE: 2004-10-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
LENGTH: 805
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                                                IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDNETEINF
                                                                                                               LLKQALTIVGTLPFTYMLEKWRWMVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETYC
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                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10957880
Publication No. US20050282154A1
GENERAL INFORMATION:
APPLICANT: Brigham & Women's Hospital, Inc.
APPLICANT: Farzan, Michael R
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Best Local Similarity 100.
Matches 595, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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US-10-957-880-1
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SACRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: SACRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING
FILE REFERENCE: 39870-3330R1C300C1
CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT PILING DATE: 2004-10-22
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2001-12-19
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-06-16
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
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PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED
                                                   139 QECLILEPGINEIMANSLDYNERLWAWESWRSEVGKQLRPLYEFYVUKNEMARANHYED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 DPASLFHVSDDYSFIRYYTRTLYQPQFQEALCQAAKHBGPLHKCDISNSTEAGQKL 554
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Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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NUMBER OF SEQ ID NO
SEQ ID NO 72
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US-10-973-115B-72
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APPLICANT:
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APPLICANT:
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APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330RG1028
CURRENT APPLICATION NUMBER: 06/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PLILING DATE: 1997-09-17
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481 SLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTEAGQKLFNMLRLG 540
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                                                                                 544 KSEPWTLALENVVGAKNMNVRPLLNYPEPLFTWLKDQNKNSFVGWSTDWSPY
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                                                                                                                                                                                                                               Sequence 72, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart, Timothy A.
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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DeForge, Laura
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ORGANISM: Homo Sapien
                                                                                                                                                                              RESULT 4
US-10-131-826A-72
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APPLICANT:
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APPLICANT:
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QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
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                                                     SLIEEKAESFLNKFNQEAEDLSYQSSLASWNYNTNITEENAQKMNEAAAKWSAFYEEQSK 78
                                                                                                                                                           439 LLKQALTIVGTLPFTYMLEKWRMVFQDKIPREQWTKKWEMKREIVGVVEPLPHDETYC
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                                                                                                                              61 LAOMYPLOEIQNLTVKLOLOALQQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNP
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                          STIEEQAKTFLDKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNNAGDKWSAFLKEQST
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84.2%; Pred. No. 3.2e-214;
ive 37; Mismatches 57;
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APPLICANT: CRACKOWER, MICHAEL A.
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREA'
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREA'
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREA'
TITLE OF INVENTION: ACE2 ACTIVATION FOR TREA'
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: CT/CA03/00882
PRIOR APPLICATION NUMBER: US 60/389,709
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENT VETSION 3.1
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| Publication No. US2005025187341
| GENERAL INFORMATION:
| APPLICANT: PENNINGER, JOSEPH M. APPLICANT: PENNINGER, MICHAEL A. ITILE OF INVENTION: ACES ACTIVATION FOR TREATMENT OF HEART, LUNG AND TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION FILE REFERENCE: SONN:064US | CURRENT PILLNG DATE: 2004-12-17 | PRIOR PILLING DATE: 2004-12-17 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING DATE: 2003-06-19 | PRIOR PILLING PILLING PILLING PILLING PILLING PILLING PILLING PILLING PILLING PILLIN
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                                                                                                                        Query Match 89.7%; Score 2897; DB 6; Best Local Similarity 99.8%; Pred. No. 6.7e-226; Matches 535; Conservative 1; Mismatches 0;
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Best Local Similarity 84.2
Matches 501; Conservative
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CORGANISM: Rattus rattus
US-10-518-599-24
                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-973-1158-72
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DEFECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NOWHER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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VCNPDNPQECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMA
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41.3%; Score 1335; DB 6; Length 7;
Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202; Indels
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; ORGANISM: Homo
US-10-995-561-1020
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US-10-995-561-1020
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                      QECLLLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNEMARANHYED 180
                                                                                                   YGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTPEEIKPLYEHLHAYVRAKLMNAYPSYISP 240
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Fublication No. US20050251873A1
GENERAL INFORMATION:
APPLICANT: PERNINGER, JOSEPH M.
APPLICANT: PERNINGER, MICHAEL A.
TITLE OF INVERTION: ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TITLE OF INVERTION ACEZ ACTIVATION FOR TREATMENT OF HEART, LUNG AND TITLE OF INVERTION ACHOES DISEASE AND HYPERTENSION
FILE REPERENCE: SONN:064US
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT APPLICATION NUMBER: US 60/389,709
FRIOR FILING DATE: 2002-06-19
FRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3:1
SEQ ID NO 23
LENGTH: 732
                                                                                                                                                                            199 YGDYWRGDYBAEGADGYNYNRNQLIEDVERTFAEIKPLYEHLHAYVRRKLMDTYPSYISP
                                                                                                                                                                                                                                                         259 IGCLPAHLLGDMWGRFWINLYPLIVPFAQKPNIDVIDAMMNQGWDAERIFQEAEKFVSV
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    LAQMYPLQE1QNLTVKLQLQALQQNGSSVLSEDKSKRLNT1LNTMST1YSTGKVCNPDNP
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41.3%; Score 1335; DB 6;
Best Local Similarity 41.9%; Pred. No. 1.1e-99;
Matches 254; Conservative 116; Mismatches 202;
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ORGANISM: Homo mapienm
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US-10-518-599-23
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Sequence 1024, Application US/10995561
Publication No. US20050272054A1
GRNERAL INFORMATION:
APPLICAMT: CARGILL, Michele et al.
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                  957 PVPRTQGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKE 1016
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                                                                                                                                     352 LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ
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41.3%; Score 1335; DB 6;
Best Local Similarity 41.9%; Pred. No. 2.3e-99;
Matches 254; Conservative 116; Mismatches 202;
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ORGANISM: Homo sapiens
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US-10-995-561-1024
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                    349
                                                                                                                                   293 AEKFFVSVGLPNMTQGFWENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVTMDDF 351
                                                                                                                                                       LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQ 411
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                 240 RLNGYVDAGDSWRSMYETPSLE------ODLERLFQELQPLYLNLHAYVRRALHRH
                                                                                  529 PVPRTGGDFDPGAKFHIPSSVPYIRYFVSFIIQFQFHEALCGAAGHTGPLHKCDIYQSKE
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                                                                  234 Y-PSYISPIGCLPAHLLGDMWGRFWTNLYSLTVPFGOKPNIDVTDAMVDQAWDAQRIFKE
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41.3%; Score 1335; DB 6;
Best Local Similarity 41.9%; Pred. No. 2e-99;
Matches 254; Conservative 116; Mismatches 202;
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CORGANISM: Homo sapiens
US-10-995-561-1019
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US-10-995-561-1019
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LTAHHEMGHIQYDMAYAAQPFLLRNGANEGFHEAVGBIMSLSAATPRHLKSIGLLSPDFQ 411
                                                                                                                                                                                                                                                                                                                        PVPHDBTYCDPASLFHVSNDYSFIRYYTRTLYQFQFQEALCQAAKHEGPLHKCDISNSTE
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41.3%; Score 1334; DB 6; Length 7
Best Local Similarity 42.6%; Pred. No. 1.3e-99;
Matches 255; Conservative 112; Mismatches 213; Indels
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APPLICANT: CRACKOWER, MICHAEL A.
TITLE OF INVENTION: ACB2 ACTIVATION FOR TREATMENT OF HEAL
TITLE OF INVENTION: KIDNEY DISEASE AND HYPERTENSION
FILE REPERENCE: SONN: 064US
CURRENT APPLICATION NUMBER: US/10/518,599
CURRENT APPLICATION NUMBER: PCT/CA03/00882
PRIOR APPLICATION NUMBER: PCT/CA03/00882
PRIOR PILING DATE: 2003-06-19
PRIOR FILING DATE: 2002-06-19
NUMBER: PSECTION OF SECTION OF SECTION NUMBER: US SOFTWARE: PROPERTY OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF S
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CORGANISM: Mus musculus
US-10-518-599-22
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL,
Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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41.3%; Score 1335; DB 6; Length 1306;
Best Local Similarity 41.9%; Pred. No. 2.4e-99;
Matches 254; Conservative 116; Mismatches 202; Indels 34;
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CRGANISM: Homo sapiens
US-10-995-561-1027
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538 NMLRLGKSEPWTLALENVVGAKNMNVRPLLNYFEPLFTWLKDQNK--NSFVGW-STDWSP
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ne : 14.1176 secs
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US-10-995-561-1022
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LENGTH: 616
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 118
  419
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                                                                                                         FLLKQALTIVGTLPFTYMLEKWRWVFKGEIPKDQWMKKWWEMKREIVGVVEPVPHDETY 479
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                              417 HIQYFMQYKDLPVTFREGANPGFHEAIGDIMALSVSTPKHLYSLNLLSTE-GSGYEYDIN
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Publication No. US20050272054A1
GENERAL INFORMATION:
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US-10-995-561-1018
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Best Local Similarity
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Sequence 1022, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT PILITING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 39.3%; Score 1269; DB 6; Length 6 Local Similarity 43.9%; Pred. No. 1.8e-94; Los 237; Conservative 100; Mismatches 185; Indels
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